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OM protein - protein search, using sw model

Run on: July 10, 2002, 09:20:34 ; Search time 29.93 Seconds
(without alignments)
29.689 Million cell updates/sec

Title: US-09-461-061a-1
Perfect score: 45
Sequence: 1 NNATFYFK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues 747574
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
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18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------------------|
| 1 | 45 | 100.0 | 9 | 21 | AA1987455 Human kininogen D3 |
| 2 | 45 | 100.0 | 10 | 21 | AA1985405 Anti-angiogenic D3 |
| 3 | 45 | 100.0 | 16 | 21 | AA198409 Anti-angiogenic D3 |
| 4 | 45 | 100.0 | 16 | 21 | AA198410 Anti-angiogenic D3 |
| 5 | 45 | 100.0 | 32 | 21 | AA198408 Anti-angiogenic D3 |
| 6 | 45 | 100.0 | 117 | 14 | AA1983350 Domaine 3, bradyki |
| 7 | 45 | 100.0 | 122 | 21 | AA1983477 Human kininogen D3 |
| 8 | 45 | 100.0 | 123 | 21 | AA1984426 Human high mol.wt. |
| 9 | 45 | 100.0 | 248 | 22 | ABG21102 Novel human diagno |
| 10 | 45 | 100.0 | 369 | 22 | ABG21099 Novel human diagno |
| 11 | 45 | 100.0 | 644 | 22 | ABG21101 Novel human diagno |

| | | | | | | |
|----|----|------|------|----|----------|--------------------|
| 12 | 39 | 86.7 | 26 | 18 | AAW54336 | Bradykinin analogo |
| 13 | 36 | 80.0 | 78 | 22 | AAO05080 | Human polypeptide |
| 14 | 34 | 75.6 | 42 | 22 | AAG74378 | Human colon cancer |
| 15 | 34 | 75.6 | 376 | 21 | AB28404 | Staphylococcus hom |
| 16 | 34 | 75.6 | 541 | 22 | AB52487 | Escherichia coli p |
| 17 | 34 | 75.6 | 602 | 20 | AAW93820 | Bacillus sp. GUS p |
| 18 | 34 | 75.6 | 602 | 20 | AAW93822 | Bacillus sp. GUS p |
| 19 | 34 | 75.6 | 602 | 20 | AAW93825 | Bacillus sp. codon |
| 20 | 34 | 75.6 | 602 | 20 | AAW93826 | Bacillus sp. GUS p |
| 21 | 34 | 75.6 | 602 | 21 | AAW28402 | Staphylococcus bet |
| 22 | 34 | 75.6 | 615 | 21 | AB28408 | Codon-optimised St |
| 23 | 34 | 75.6 | 618 | 20 | AAW93821 | Bacillus sp. GUS p |
| 24 | 33 | 73.3 | 71 | 22 | AAW82831 | Human immune/haema |
| 25 | 33 | 73.3 | 173 | 21 | AAG44316 | Arabidopsis thalia |
| 26 | 33 | 73.3 | 251 | 21 | AAG44315 | Arabidopsis thalia |
| 27 | 33 | 73.3 | 259 | 21 | AAG44314 | Arabidopsis thalia |
| 28 | 32 | 71.1 | 1191 | 22 | AB260775 | Drosophila melanog |
| 29 | 31 | 68.9 | 67 | 21 | AB34049 | Human secreted pro |
| 30 | 31 | 68.9 | 77 | 22 | AAW84819 | Human immune/haema |
| 31 | 31 | 68.9 | 89 | 21 | AAG01238 | Human secreted pro |
| 32 | 31 | 68.9 | 121 | 21 | AAW81200 | Human mutant cysta |
| 33 | 31 | 68.9 | 128 | 21 | AAW81189 | Human mutant cysta |
| 34 | 31 | 68.9 | 149 | 20 | AAW35862 | Protein which is s |
| 35 | 31 | 68.9 | 161 | 22 | AAO12964 | Human polypeptide |
| 36 | 31 | 68.9 | 178 | 22 | ABG09760 | Novel human diagno |
| 37 | 31 | 68.9 | 193 | 16 | AAW71919 | Macaque platelet a |
| 38 | 31 | 68.9 | 193 | 18 | AAW26505 | Macaque platelet a |
| 39 | 31 | 68.9 | 193 | 18 | AAW23800 | Macaque partial pl |
| 40 | 31 | 68.9 | 193 | 18 | AAW09812 | Partial macaque pl |
| 41 | 31 | 68.9 | 193 | 19 | AAW38365 | Monkey plasma plat |
| 42 | 31 | 68.9 | 193 | 20 | AAW96340 | Internal PAF-AH pe |
| 43 | 31 | 68.9 | 193 | 20 | AAW73365 | Macaque PAF-AH pe |
| 44 | 31 | 68.9 | 193 | 21 | AAW07996 | A macaque platelet |
| 45 | 31 | 68.9 | 193 | 21 | AAW88310 | Macaque PAF-AH ami |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | |
| AAW37455 | |
| ID | AAW37455 standard; peptide; 9 AA. |
| AC | AAW37455; |
| DT | 21-FEB-2001 (first entry) |
| DE | Human kininogen D3 peptide fragment. |
| KW | Enzyme; legumain; endopeptidase; cystatin; human; kininogen. |
| OS | Homo sapiens. |
| PN | WO2000064945-A1. |
| PD | 02-NOV-2000. |
| PF | 20-APR-2000; 2000WO-GB01571. |
| PR | 22-APR-1999; 99GB-0009133. |
| XX | (BABR-) BABRAHAM INST. |
| XX | Abrahamson M, Barrett AJ; |
| XX | WPI; 2000-687316/67. |
| XX | Inhibition of mammalian legumain or legumain-related endopeptidase by |
| XX | cystatin involves interaction with second papain-non-reactive site of |
| XX | cystatin - |
| XX | Disclosure: Fig 4; 45pp; English. |

CC The present invention relates to inhibition of the enzymatic activity of
 CC legumain or a legumain-related endopeptidase by cystatin. The inhibition
 CC involves an interaction between legumain and a papain-non-reactive site
 CC of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and
 CC performs a protein-processing function. The present sequence is a peptide
 CC fragment of human kininogen D3, which was used in the present invention.
 CC Kininogen is a type 3 cystatin. The present sequence is thought to be
 CC involved in a legumain-inhibitory site.

XX Sequence 9 AA;

Query Match 100.0%; Score 45; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFFYFK 8
 Db 1 nnatfyfk 8

RESULT 2

AAV95405
 ID AAV95405 standard; Peptide; 10 AA.

XX AC AAV95405;

XX 25-SEP-2000 (first entry)

XX Anti-angiogenic D3 peptide.

XX Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
 XX endothelial cell proliferation; apoptosis; cancer; ocular disorder;
 XX rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
 XX therapy; human; D3 peptide.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Xaa represents 0 amino acids, or the
 FT sequence of AAV95406 or its N-terminal
 FT truncation fragment containing at least
 FT 1 amino acid"

FT Peptide 2..9 /note= "corresponds to residues Asn(275)-Lys(282)
 FT of HK domain 3"

FT Misc-difference 10 /note= "Xaa represents 0 amino acids, or the
 FT sequence of AAV95407 or its C-terminal
 FT truncation fragment containing at least
 FT 1 amino acid"

XX WO200035407-A2.

XX 22-JUN-2000.

XX 02-DEC-1999; 99WO-US28465.

XX 16-DEC-1998; 98US-0112427.

XX (UTEM) UNIV TEMPLE.

XX (MCCR/) MCCRAE R K.

XX McCrae RK;

XX WPI; 2000-442247/38.

XX Composition for inhibiting angiogenesis and endothelial cell
 XX proliferation, inducing endothelial cell apoptosis and treating cancer,
 XX rheumatoid arthritis, and ocular disorders comprises a kininogen domain
 XX 3 analog

PS Claim 1; Page 25; 44pp; English.

XX The present sequence is that of a D3 peptide derived from high
 CC mol.wt. kininogen (HK) domain 3 (see AAV95426). The D3 peptide, which
 CC may optionally include N-terminal and/or C-terminal protecting
 CC groups, inhibits endothelial cell proliferation and thus possesses
 CC anti-angiogenic activity. It is an example of peptides of the
 CC invention (see AAV95405-26) which are analogues of certain sites in
 CC the HK domain 3, in this case amino acids Asn275-Lys282. The
 CC peptides inhibit endothelial cell proliferation and may also induce
 CC endothelial cell apoptosis. Compositions including such peptides
 CC are used in claimed methods for inhibiting angiogenesis, inhibiting
 CC endothelial cell proliferation, and inducing endothelial cell
 CC apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
 CC characterized by undesired vascularization of the retina are treated.

XX Sequence 10 AA;

Query Match 100.0%; Score 45; DB 21; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.051;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFFYFK 8
 Db 2 nnatfyfk 9

RESULT 3

AAV95409

ID AAV95409 standard; Peptide; 16 AA.

XX AC AAV95409;

XX 25-SEP-2000 (first entry)

XX Anti-angiogenic D3 peptide.

XX Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
 XX endothelial cell proliferation; apoptosis; cancer; ocular disorder;
 XX rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
 XX therapy; human; D3 peptide.

XX OS Homo sapiens.

XX WO200035407-A2.

XX 22-JUN-2000.

XX 02-DEC-1999; 99WO-US28465.

XX 16-DEC-1998; 98US-0112427.

XX (UTEM) UNIV TEMPLE.

XX (MCCR/) MCCRAE R K.

XX McCrae RK;

XX WPI; 2000-442247/38.

XX Composition for inhibiting angiogenesis and endothelial cell
 XX proliferation, inducing endothelial cell apoptosis and treating cancer,
 XX rheumatoid arthritis, and ocular disorders comprises a kininogen domain
 XX 3 analog

PS Claim 6; Page 26; 44pp; English.

XX The present sequence is that of a D3 peptide derived from human
 CC high mol.wt. kininogen (HK) domain 3 (see AAV95426). The D3 peptide
 CC inhibits endothelial cell proliferation and thus possesses of the
 CC anti-angiogenic activity. It is an example of D3 peptides of the
 CC invention (see AAV95405-26) that are analogues of certain sites in
 CC the HK domain 3, in this case amino acid residues Asn275-Lys282.

CC The peptides inhibit endothelial cell proliferation and may also
 CC induce endothelial cell apoptosis. Compositions including the
 CC peptides are used in claimed methods for inhibiting angiogenesis,
 CC inhibiting endothelial cell proliferation, and inducing endothelial
 CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
 CC characterized by undesired vascularization of the retina are treated.
 CC The IC50 value for the present peptide was less than 0.8 μ M for
 CC inhibition of fibroblast growth factor-induced HUVEC cell
 CC proliferation.
 CC
 XX Sequence 16 AA;
 SQ

Query Match 100.0%; Score 45; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.082;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
 ID 9 nnatfyfk 16
 DB

RESULT 4
 AAY95410
 ID AAY95410 standard; Peptide; 16 AA.
 XX
 AC AAY95410;
 XX

DT 25-SEP-2000 (first entry)

DE Anti-angiogenic D3 peptide.

KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
 KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;
 KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
 KW therapy; human; D3 peptide.
 XX

OS Homo sapiens.

PN WO200035407-A2.

XX 22-JUN-2000.

PF 02-DEC-1999; 99WO-US28465.

PR 16-DEC-1998; 98US-0112427.

XX (UTEM) UNIV TEMPLE.
 PA (MCCR/) MCCRAE R K.
 XX

PI McCrae RK;

XX WPI; 2000-442247/38.

XX Composition for inhibiting angiogenesis and endothelial cell
 PT proliferation, inducing endothelial cell apoptosis and treating cancer,
 PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
 PT 3 analog -

PS Claim 7; Page 26; 44pp; English.

XX The present sequence is that of a D3 peptide derived from human
 CC high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide
 CC inhibits endothelial cell proliferation and thus possesses
 CC anti-angiogenic activity. It is an example of D3 peptides of the
 CC invention (see AAY95405-26) that are analogues of certain sites in
 CC the HK domain 3, in this case amino acid residues Asn275-Lys282.
 CC The peptides inhibit endothelial cell proliferation and may also
 CC induce endothelial cell apoptosis. Compositions including the
 CC peptides are used in claimed methods for inhibiting angiogenesis,
 CC inhibiting endothelial cell proliferation, and inducing endothelial
 CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
 CC characterized by undesired vascularization of the retina are treated.

CC The IC50 value for the present peptide was less than 0.8 μ M for
 CC inhibition of fibroblast growth factor-induced HUVEC cell
 CC proliferation.
 XX Sequence 16 AA;
 SQ

Query Match 100.0%; Score 45; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.082;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
 ID 1 nnatfyfk 8
 DB

RESULT 5
 AAY95408
 ID AAY95408 standard; Peptide; 32 AA.
 XX
 AC AAY95408;
 XX

DT 25-SEP-2000 (first entry)

DE Anti-angiogenic D3 peptide.

KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
 KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;
 KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
 KW therapy; human; D3 peptide.
 XX

OS Homo sapiens.

PN WO200035407-A2.

XX 22-JUN-2000.

PF 02-DEC-1999; 99WO-US28465.

PR 16-DEC-1998; 98US-0112427.

XX (UTEM) UNIV TEMPLE.
 PA (MCCR/) MCCRAE R K.
 XX

PI McCrae RK;

XX WPI; 2000-442247/38.

XX Composition for inhibiting angiogenesis and endothelial cell
 PT proliferation, inducing endothelial cell apoptosis and treating cancer,
 PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
 PT 3 analog -

PS Claim 4; Page 26; 44pp; English.

XX The present sequence is that of a D3 peptide derived from human
 CC high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide
 CC inhibits endothelial cell proliferation and thus possesses
 CC anti-angiogenic activity. It is an example of D3 peptides of the
 CC invention (see AAY95405-26) that are analogues of certain sites in
 CC the HK domain 3, in this case amino acid residues Asn275-Lys282.
 CC The peptides inhibit endothelial cell proliferation and may also
 CC induce endothelial cell apoptosis. Compositions including the
 CC peptides are used in claimed methods for inhibiting angiogenesis,
 CC inhibiting endothelial cell proliferation, and inducing endothelial
 CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
 CC characterized by undesired vascularization of the retina are treated.

XX Sequence 32 AA;

Query Match 100.0%; Score 45; DB 21; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
 ID AAB37447 standard; protein; 122 AA.
 XX
 XX AAB37447;
 XX
 XX 21-FEB-2001 (first entry)
 XX
 XX Human kininogen D3.
 XX
 XX Enzyme; legumain; endopeptidase; cystatin; human; kininogen.
 XX
 XX Homo sapiens.
 XX
 XX WO200064945-A1.
 XX
 XX 02-NOV-2000.
 XX
 XX 20-APR-2000; 2000WO-GB01571.
 XX
 XX 22-APR-1999; 99GB-0009133.
 XX
 XX (BABR-) BABRAHAM INST.
 XX
 XX Abrahamson M, Barrett AJ;
 XX
 XX WPI; 2000-687316/67.
 XX
 XX Inhibition of mammalian legumain or legumain-related endopeptidase by
 XX cystatin involves interaction with second papain-non-reactive site of
 XX cystatin
 XX
 XX Disclosure; Fig 4; 45pp; English.
 XX
 XX The present invention relates to inhibition of the enzymatic activity of
 XX legumain or a legumain-related endopeptidase by cystatin. The inhibition
 XX involves an interaction between legumain and a papain-non-reactive site
 XX of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and
 XX performs a protein-processing function. The present sequence is human
 XX kininogen D3, which was used in the present invention. Kininogen is a
 XX type 3 cystatin.
 XX
 XX Sequence 122 AA;
 SQ

RESULT 6

AAR33350
 ID AAR33350 standard; protein; 117 AA.
 XX
 XX AAR33350;
 XX
 XX 01-JUL-1993 (first entry)
 XX
 XX Domaine 3, bradykinin release activating peptide.
 XX
 XX Domain 3; human; kininogen; heavy chain; low molecular weight; plasma;
 XX trypsin; platelet; activation; granule contents; hemostasis; thrombin;
 XX tissue plasminogen activator; thrombosis; inflammatory response;
 XX endothelial cell; von Willebrand factor;
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..18
 XX /note= "Leader peptide"
 XX Protein 19..117
 XX /note= "Mature protein"
 XX
 XX WO9303748-A.
 XX
 XX 04-MAR-1993.
 XX
 XX 13-AUG-1992; 92WO-US06809.
 XX
 XX 13-AUG-1991; 91US-0744545.
 XX
 XX (UTEM) UNIV TEMPLE.
 XX
 XX Jiang Y, Schmaier AB;
 XX
 XX WPI; 1993-093714/11.
 XX
 XX Use of trypsin-cleavage fragment of human kininogen - for
 XX increasing vascular bradykinin release, for lowering blood
 XX pressure and treating hypertension
 XX
 XX Disclosure; Fig 1; 46pp; English.
 XX
 XX The sequence given represents domain 3, amino acids 246-362, of
 XX the human kininogen heavy chain. Domain 3 was isolated from low
 XX molecular weight kininogen, derived from human plasma, by cleavage
 XX with trypsin. Domain 3 peptide inhibits platelet activation causing
 XX a marked decrease in the platelets ability to aggregate and secrete
 XX their granule contents. The granule contents comprise proteins which
 XX participate in hemostasis, thrombosis and the inflammatory response.
 XX Domain 3 also inhibits endothelial cell activation shown by a decrease
 XX in secretion of endothelial cell contents such as tissue plasminogen
 XX activator and von Willebrand factor. Domain 3 functions to inhibit
 XX cell activation by blocking thrombin binding to its target cells, the
 XX peptide is a selective inhibitor of thrombin-induced platelet
 XX activation.
 XX
 XX Sequence 117 AA;
 SQ

Query Match 100.0%; Score 45; DB 14; Length 117;

Best Local Similarity 100.0%; Pred. No. 0.64;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
 ID AAB37447 standard; protein; 122 AA.
 XX
 XX AAB37447;
 XX
 XX 21-FEB-2001 (first entry)
 XX
 XX Human kininogen D3.
 XX
 XX Enzyme; legumain; endopeptidase; cystatin; human; kininogen.
 XX
 XX Homo sapiens.
 XX
 XX WO200064945-A1.
 XX
 XX 02-NOV-2000.
 XX
 XX 20-APR-2000; 2000WO-GB01571.
 XX
 XX 22-APR-1999; 99GB-0009133.
 XX
 XX (BABR-) BABRAHAM INST.
 XX
 XX Abrahamson M, Barrett AJ;
 XX
 XX WPI; 2000-687316/67.
 XX
 XX Inhibition of mammalian legumain or legumain-related endopeptidase by
 XX cystatin involves interaction with second papain-non-reactive site of
 XX cystatin
 XX
 XX Disclosure; Fig 4; 45pp; English.
 XX
 XX The present invention relates to inhibition of the enzymatic activity of
 XX legumain or a legumain-related endopeptidase by cystatin. The inhibition
 XX involves an interaction between legumain and a papain-non-reactive site
 XX of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and
 XX performs a protein-processing function. The present sequence is human
 XX kininogen D3, which was used in the present invention. Kininogen is a
 XX type 3 cystatin.
 XX
 XX Sequence 122 AA;
 SQ

Query Match 100.0%; Score 45; DB 21; Length 122;

Best Local Similarity 100.0%; Pred. No. 0.67;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
 ID AAB37447 standard; protein; 122 AA.
 XX
 XX AAB37447;
 XX
 XX 21-FEB-2001 (first entry)
 XX
 XX Human kininogen D3.
 XX
 XX Enzyme; legumain; endopeptidase; cystatin; human; kininogen.
 XX
 XX Homo sapiens.
 XX
 XX WO200064945-A1.
 XX
 XX 02-NOV-2000.
 XX
 XX 20-APR-2000; 2000WO-GB01571.
 XX
 XX 22-APR-1999; 99GB-0009133.
 XX
 XX (BABR-) BABRAHAM INST.
 XX
 XX Abrahamson M, Barrett AJ;
 XX
 XX WPI; 2000-687316/67.
 XX
 XX Inhibition of mammalian legumain or legumain-related endopeptidase by
 XX cystatin involves interaction with second papain-non-reactive site of
 XX cystatin
 XX
 XX Disclosure; Fig 4; 45pp; English.
 XX
 XX The present invention relates to inhibition of the enzymatic activity of
 XX legumain or a legumain-related endopeptidase by cystatin. The inhibition
 XX involves an interaction between legumain and a papain-non-reactive site
 XX of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and
 XX performs a protein-processing function. The present sequence is human
 XX kininogen D3, which was used in the present invention. Kininogen is a
 XX type 3 cystatin.
 XX
 XX Sequence 122 AA;
 SQ

RESULT 8

AAY95426
 ID AAY95426 standard; Peptide; 123 AA.
 XX
 XX AAY95426;
 XX
 XX 25-SEP-2000 (first entry)
 XX
 XX Human high mol.wt. kininogen domain 3.
 XX
 XX Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
 XX endothelial cell proliferation; apoptosis; cancer; ocular disorder;
 XX rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
 XX therapy; human; D3 peptide.
 XX
 XX Homo sapiens.
 XX

XX PN WO200035407-A2.
XX PD 22-JUN-2000.
XX PF 02-DEC-1999; 99WO-US28465.
XX PR 16-DEC-1998; 98US-0112427.
XX PA (UTEM) UNIV TEMPLE.
XX PA (MCCR/) MCCRAE R K.
XX PI McCrae RK;
XX DR WPI; 2000-442247/38.
XX PT Composition for inhibiting angiogenesis and endothelial cell
PT proliferation, inducing endothelial cell apoptosis and treating cancer,
PT 3 analog -
XX PS Disclosure; Page 4; 44pp; English.
XX CC The present sequence is that of domain 3 of human high mol.wt.
CC kininogen (HK). The invention provides peptides (see AAY95405-24)
CC that are analogues of certain sites in the HK domain 3,
CC specifically Asn275-Lys282, Cys246-Cys249, Leu331-Tyr338 and
CC Tyr299-Ser314. The peptides, in which native Cys residues may be
CC replaced by Ala residues, inhibit endothelial cell proliferation
CC and may also induce endothelial cell apoptosis. Compositions
CC including the peptides are used in claimed methods for inhibiting
CC angiogenesis, inhibiting endothelial cell proliferation, and
CC inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis,
CC and ocular disorders characterized by undesired vascularization of
CC the retina are treated.
XX SQ Sequence 123 AA;

Query Match 100.0%; Score 45; DB 21; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
|||||||
Db 41 nnatfyfk 48

RESULT 9
ABG21102
ID ABG21102 standard; Protein; 248 AA.
XX AC ABG21102;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #21093.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS85289.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX PS Claim 20; SEQ ID No 51461; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 248 AA;

Query Match 100.0%; Score 45; DB 22; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
|||||||
Db 90 nnatfyfk 97

RESULT 10
ABG21099
ID ABG21099 standard; Protein; 369 AA.
XX AC ABG21099;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #21090.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;
 XX WPI: 2001-639362/73.
 DR N-PSDB; AAS85286.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 20; SEQ ID No 51458; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 369 AA;

Query Match 100.0%; Score 45; DB 22; Length 369;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFFK 8
 |||||
 Db 333 nnatfyfk 340

RESULT 11
 ABG21101
 ID ABG21101 standard; Protein: 644 AA.
 XX
 AC ABG21101;
 DT
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #21092.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.
 DR N-PSDB; AAS85288.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 20; SEQ ID No 51460; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 644 AA;

Query Match 100.0%; Score 45; DB 22; Length 644;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFFK 8
 |||||
 Db 293 nnatfyfk 300

RESULT 12
 AAW54336
 ID AAW54336 standard; peptide: 26 AA.
 XX
 AC AAW54336;

DT 30-JUL-1998 (first entry)
 XX
 DE Bradykinin analogous peptide 19.

XX Inhibition; thrombin-induced platelet; prevention; platelet aggregation;
 KW ADP-induced activation.
 XX
 OS Synthetic.

XX WO9641640-A1.
 PN
 PD 27-DEC-1996.

XX 07-JUN-1996; 96WO-US09940.
 XX
 PR 09-JUN-1995; 95US-0000096.
 XX
 PA (UNMI) UNIV MICHIGAN.

XX Hasan AAK, Schmaier AH;
 XX WPI: 1997-065304/06.
 DR

XX Inhibition of platelet activation and aggregation - by admin. of new
PT or known bradykinin analogues
XX Disclosure; Page 44; 73pp; English.
XX
CC Administration of a peptide or multimer related to bradykinin or other
CC disclosed peptides and multimers can be used for the inhibition of
CC thrombin-induced platelets or other cells. They can also be used for
CC preventing platelet aggregation, or inhibiting ADP-induced activation.
CC This is useful to prevent arterial occlusions arising from coronary
CC thrombosis and stroke.
XX Sequence 26 AA;
SQ

Query Match 86.7%; Score 39; DB 18; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFYFK 8
Db 1 natfyfk 7
IIIIII

RESULT 13
AAO05080
ID AAO05080 standard; Protein; 78 AA.
XX AC AAO05080;
XX
XX 06-NOV-2001 (first entry)
XX Human polypeptide SEQ ID NO 18972.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX Homo sapiens.
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
XX 18-MAY-2000; 2000US-0577409.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
XX N-PSDB; AAI85011.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
XX diagnosing and treating e.g. leukaemia, inflammation and immune
XX disorders -
XX
XX Claim 20; SEQ ID NO 18972; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 78 AA;
Query Match 80.0%; Score 36; DB 22; Length 78;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYF 7
Db 38 nnttfyf 44
IIIIII

RESULT 14
AAG74378
ID AAG74378 standard; Protein; 42 AA.
XX AC AAG74378;
XX
XX 03-SEP-2001 (first entry)
XX Human colon cancer antigen protein SEQ ID NO:5142.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma.
XX Homo sapiens.
XX WO200122920-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000WO-US26524.
XX
XX 29-SEP-1999; 99US-0157137.
XX 03-NOV-1999; 99US-0163280.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX WPI; 2001-235357/24.
XX N-PSDB; AAI33809.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX Claim 11; Page 6843; 9803pp; English.
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where
XX the proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene
XX therapy and vaccine production. N and P may be used in the prevention,
XX diagnosis and treatment of diseases associated with inappropriate P
XX expression. For example, N and P may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of P by expressing P.
XX inactive proteins or to supplement the patients own production of P.
XX Additionally, N may be used to produce the colon cancer-associated Ps,
XX by inserting the nucleic acids into a host cell and culturing the cell
XX to express the proteins. N and P can be used in the prevention, diagnosis
XX and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
XX and AAH77789 represent sequences used in the exemplification of the
XX present invention.
XX
XX N.B. Pages 666 to 682 and page 7053 of the sequence listing were
XX missing at time of publication, meaning no sequences are present for
XX SEQ ID NO:1027 to 1052, 7921 and 7922.

XX SQ Sequence 42 AA;

Query Match 75.6%; Score 34; DB 22; Length 42;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFYF 7
| | | | |
Db 22 nratfyf 28

RESULT 15

AAE28404
ID AAB28404 standard; Protein; 376 AA.

XX AC AAB28404;

XX DT 26-JAN-2001 (first entry)

XX DE Staphylococcus homini beta-D-glucuronidase.

XX KW Microbial; beta-glucuronidase; GUS; Enterobacter; Salmonella;

XX KW Pseudomonas; Staphylococcus; Thermotoga; transgenic plant; bioindicator;
transgenic insect; marker; glucuronide detoxification.

XX OS Staphylococcus homini.

XX PN WO200055333-A1.

XX PD 21-SEP-2000.

XX PF 16-MAR-2000; 2000WO-US07107.

XX PR 17-MAR-1999; 99US-0270957.

XX PA (CMB-) CAMBIA BIOSYSTEMS LLC.

XX PI Jefferson RA, Mayer JE;

XX DR WPI; 2000-647075/62.

XX DR N-PSDB; AAA07936.

XX PT Novel microbial beta-glucuronidase genes and gene products used as
reporter/effector molecule, as diagnostic tool, in positive selection,
to target molecules to specific cells and to detect and track linked
genes -

XX Claim 3; Fig 5B; 116pp; English.

XX The present sequence is a microbial beta-glucuronidase (GUS)

XX protein. GUS genes were obtained from six different genera:

XX Enterobacter/Salmonella, Pseudomonas, Salmonella, Staphylococcus and

XX Thermotoga. Microbial GUS can be used as a reporter/effector molecule for

XX transgenic constructions and in vitro diagnostic applications. It may

XX also be used to generate sentinel plants that serve as bioindicators of

XX environmental status. It may be used to generate transgenic insects for

XX tracking insect populations or to facilitate the development of a

XX bioassay for compounds that affect molecules critical for insect

XX development (e.g. juvenile hormone). Secreted GUS may also serve as a

XX marker for beneficial fungi destined for release into the environment. In

XX animal systems, secreted GUS may be used to achieve extracellular

XX detoxification of glucuronides (e.g. toxin glucuronide) and to examine

XX conjugation patterns of glucuronides. Microbial GUS may also be used in

XX traditional medical diagnostic assays, for drug testing, pharmacokinetic

XX studies, bioavailability studies, diagnosis of diseases and syndromes,

XX following progression of disease or its response to therapy. Microbial

XX GUS has increased thermal stability, high turnover number and enzymatic

XX activity. It is highly specific for the substrate and water soluble, and

XX the substrates are stable.

XX Sequence 376 AA;

Query Match 75.6%; Score 34; DB 21; Length 376;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
| | | | |
Db 57 nnkpfyfk 64

Search completed: July 10, 2002, 09:21:54
Job time: 80 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2002, 09:20:34 ; Search time 13.1 Seconds
(without alignments)
14.916 Million cell updates/sec

Title: US-09-461-061a-1
Perfect score: 45
Sequence: 1 NNATFFVK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCRTUS_COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 45 | 100.0 | 117 | 1 | US-08-193-114B-1 |
| 2 | 45 | 100.0 | 117 | 5 | PCT-US92-06809-1 |
| 3 | 39 | 86.7 | 26 | 4 | US-08-676-242-15 |
| 4 | 31 | 68.9 | 193 | 1 | US-08-483-140-30 |
| 5 | 31 | 68.9 | 193 | 2 | US-08-483-938A-36 |
| 6 | 31 | 68.9 | 441 | 1 | US-08-470-187-8 |
| 7 | 31 | 68.9 | 441 | 1 | US-08-318-905-8 |
| 8 | 31 | 68.9 | 441 | 1 | US-08-483-232-8 |
| 9 | 31 | 68.9 | 441 | 1 | US-08-483-140-8 |
| 10 | 31 | 68.9 | 441 | 2 | US-08-485-938A-8 |
| 11 | 31 | 68.9 | 441 | 2 | US-08-910-041-8 |
| 12 | 31 | 68.9 | 441 | 3 | US-09-328-474-8 |
| 13 | 31 | 68.9 | 441 | 3 | US-09-100-546-8 |
| 14 | 31 | 68.9 | 441 | 4 | US-09-010-715-8 |
| 15 | 31 | 68.9 | 441 | 4 | US-09-577-758-8 |
| 16 | 31 | 68.9 | 444 | 1 | US-08-483-140-28 |
| 17 | 31 | 68.9 | 444 | 2 | US-08-485-938A-32 |
| 18 | 31 | 68.9 | 902 | 1 | US-08-701-846-2 |
| 19 | 31 | 68.9 | 2710 | 1 | US-08-480-604A-6 |
| 20 | 31 | 68.9 | 2710 | 2 | US-08-405-496A-6 |
| 21 | 31 | 68.9 | 2710 | 4 | US-08-915-136-6 |
| 22 | 30 | 66.7 | 84 | 4 | US-09-227-357-597 |
| 23 | 30 | 66.7 | 572 | 6 | 5200183-5 |
| 24 | 30 | 66.7 | 602 | 3 | US-08-446-100-1 |
| 25 | 30 | 66.7 | 602 | 3 | US-08-446-100-2 |
| 26 | 30 | 66.7 | 602 | 3 | US-08-446-100-3 |
| 27 | 30 | 66.7 | 602 | 3 | US-08-446-100-4 |

| | | | | | | |
|----|----|------|-----|---|------------------|--------------------|
| 28 | 30 | 66.7 | 602 | 3 | US-08-446-100-5 | Sequence 5, Appl |
| 29 | 30 | 66.7 | 602 | 3 | US-08-446-100-6 | Sequence 6, Appl |
| 30 | 30 | 66.7 | 602 | 3 | US-08-446-100-7 | Sequence 7, Appl |
| 31 | 30 | 66.7 | 602 | 3 | US-08-446-100-8 | Sequence 8, Appl |
| 32 | 30 | 66.7 | 602 | 3 | US-08-446-100-9 | Sequence 9, Appl |
| 33 | 30 | 66.7 | 602 | 3 | US-08-446-100-10 | Sequence 10, Appl |
| 34 | 30 | 66.7 | 602 | 3 | US-08-446-100-11 | Sequence 11, Appl |
| 35 | 30 | 66.7 | 602 | 3 | US-08-446-100-12 | Sequence 12, Appl |
| 36 | 30 | 66.7 | 602 | 3 | US-08-446-100-13 | Sequence 13, Appl |
| 37 | 30 | 66.7 | 602 | 3 | US-08-446-100-14 | Sequence 14, Appl |
| 38 | 30 | 66.7 | 602 | 3 | US-08-446-100-15 | Sequence 15, Appl |
| 39 | 30 | 66.7 | 602 | 3 | US-08-446-100-16 | Sequence 16, Appl |
| 40 | 30 | 66.7 | 602 | 3 | US-08-446-100-17 | Sequence 17, Appl |
| 41 | 30 | 66.7 | 602 | 3 | US-08-446-100-18 | Sequence 18, Appl |
| 42 | 30 | 66.7 | 602 | 3 | US-08-446-100-24 | Sequence 24, Appl |
| 43 | 30 | 66.7 | 602 | 4 | US-09-334-489-3 | Sequence 3, Appl |
| 44 | 30 | 66.7 | 602 | 4 | US-09-334-489-4 | Sequence 4, Appl |
| 45 | 30 | 66.7 | 602 | 6 | 5215909-11 | Patent No. 5215909 |

ALIGNMENTS

RESULT 1
US-08-193-114B-1
: Sequence 1, Application US/08193114B
: Patent No. 5472945
: GENERAL INFORMATION:
: APPLICANT: Schmaier, Alvin H.
: APPLICANT: Jiang, Yongping
: TITLE OF INVENTION: Modulation of Blood
: TITLE OF INVENTION: Pressure and Inhibition of Platelet Activation
: TITLE OF INVENTION: with Kininogen Fragment
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seidel, Gonda, Lavorgna &
: ADDRESSEE: Monaco, P.C.
: STREET: 1800 Two Penn Center Plaza
: CITY: Philadelphia
: STATE: Pennsylvania
: COUNTRY: U.S.A.
: ZIP: 19102
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/193,114B
: FILING DATE: 9 February 1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: U.S. Application
: APPLICATION NUMBER: Serial No. 5472945 07/744,545
: FILING DATE: 13 August 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Monaco, Daniel A.
: REGISTRATION NUMBER: 30,480
: REFERENCE/DOCKET NUMBER: 6056-137 CII
: TELEPHONE: (215) 568-8383
: TELEFAX: (215) 568-5549
: TELEX: No. 5472945e
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 117 amino acids
: TYPE: peptide
: TOPOLOGY: linear
US-08-193-114B-1

SEA ID No: 1

Query Match 100.0%; Score 45; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
|||||||
Db 30 NNATFYFK 37

RESULT 2

PCT-US92-06809-1
; Sequence 1, Application PC/TUS9206809
; GENERAL INFORMATION:
; APPLICANT: Schmaier, Alvin H.
; APPLICANT: Jiang, Yongping
; TITLE OF INVENTION: Modulation of Blood
; TITLE OF INVENTION: Pressure by Altering Bradykinin Levels
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of the
; ADDRESSEE: Commonwealth System of Higher Education
; STREET: 406 University Services
; STREET: Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/06809

; FILING DATE: 19910813

; CLASSIFICATION: 514

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. Application

; APPLICATION NUMBER: Serial No. 744,545

; FILING DATE: 13 August 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Monaco, Daniel A.

; REGISTRATION NUMBER: 30,480

; REFERENCE/DOCKET NUMBER: 6056-137

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-8383

; TELEFAX: (215) 568-5549

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

PCT-US92-06809-1

Query Match 100.0%; Score 45; DB 5; Length 117;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
|||||||
Db 30 NNATFYFK 37

RESULT 3

US-08-676-242-15
; Sequence 15, Application US/08676242C
; Patent No. 6143719

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of Michigan

; APPLICANT: Schmaier, Alvin H.

; APPLICANT: Hasan, Ahmed A.K.

; TITLE OF INVENTION: Bradykinin Analogs As Selective Thrombin Inhibitors

; FILE REFERENCE: 8820-2 US

; CURRENT APPLICATION NUMBER: US/08/676,242C
; CURRENT FILING DATE: 2000-07-16
; EARLIER APPLICATION NUMBER: 60/000,096
; EARLIER FILING DATE: 1995-06-09
; EARLIER APPLICATION NUMBER: PCT/US96/09940
; EARLIER FILING DATE: 1996-06-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bradykinin
; OTHER INFORMATION: analog
US-08-676-242-15

Query Match 86.7%; Score 39; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFYFK 8
|||||||
Db 1 NATFYFK 7

RESULT 4

US-08-483-140-30

; Sequence 30, Application US/08483140

; Patent No. 5698403

; GENERAL INFORMATION:

; APPLICANT: ICOS Corporation

; TITLE OF INVENTION: Platelet-Activating Factor Acetyl

; TITLE OF INVENTION: Hydrolase

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,140

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/318,905

; FILING DATE: 6-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/133,803

; FILING DATE: 6-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5698403and, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 32781

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3658

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 193 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-483-140-30

Query Match 68.9%; Score 31; DB 1; Length 193;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATYFK 8
: : : : :
Db 143 SATYFK 149

RESULT 5
US-08-485-938A-36
; Sequence 36, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA: US 08/133,803
; APPLICATION NUMBER: 06-OCT-1993
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-0448
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-938A-36

Query Match 68.9%; Score 31; DB 2; Length 193;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATYFK 8
: : : : :
Db 143 SATYFK 149

RESULT 6
US-08-470-187-8
; Sequence 8, Application US/08470187
; Patent No. 5532152
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine E.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532152and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-470-187-8

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATYFK 8
: : : : :
Db 185 SATYFK 191

RESULT 7
US-08-318-905-8
; Sequence 8, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,905
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 564169and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-905-8

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATFYFK 8
:|:|:|
Db 185 SATYFK 191

RESULT 8
US-08-483-232-8
Sequence 8, Application US/08483232
Patent No. 5656431
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,232
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 565643land, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32689
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-232-8

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATFYFK 8
:|:|:|
Db 185 SATYFK 191

RESULT 9
US-08-483-140-8
Sequence 8, Application US/08483140
Patent No. 5698403
GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,140
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 6-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5698403and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-140-8

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFYFK 8
Db 185 SATYFK 191

RESULT 10

US-08-485-938A-8
; Sequence 8, Application US/08485938A
; Patent No. 5847088

; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-938A-8

Query Match 68.9%; Score 31; DB 2; Length 441;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFYFK 8
Db 185 SATYFK 191

RESULT 11

US-08-910-041-8
; Sequence 8, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,041
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-910-041-8

Query Match 68.9%; Score 31; DB 2; Length 441;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFYFK 8
Db 185 SATYFK 191

RESULT 12
US-09-328-474-8

; Sequence 8, Application US/09328474
; Patent No. 6045794
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-328-474-8

Query Match 68.9%; Score 31; DB 3; Length 441;
Best Local Similarity 71.4%; Pred. NO. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATFYFK 8
Db 185 SATYFK 191

RESULT 13
US-09-100-546-8
; Sequence 8, Application US/09100546
; Patent No. 6099836
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.

; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6099836and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-100-546-8

Query Match 68.9%; Score 31; DB 3; Length 441;
Best Local Similarity 71.4%; Pred. NO. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATFYFK 8
Db 185 SATYFK 191

RESULT 14
US-09-010-715-8
; Sequence 8, Application US/09010715
; Patent No. 6146625
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois

; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 614662sand, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-010-715-8

Query Match 68.9%; Score 31; DB 4; Length 441;
Best Local Similarity 71.4%; Pred. NO. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATVEFK 8
Db 185 SATYVFK 191

RESULT 15
US-09-577-758-8
; Sequence 8, Application US/09577758
; Patent No. 6203790
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,758
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/010,715
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6203790and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-577-758-8

Query Match 68.9%; Score 31; DB 4; Length 441;
Best Local Similarity 71.4%; Pred. NO. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATVEFK 8
Db 185 SATYVFK 191

Search completed: July 10, 2002, 09:20:56
Job time: 22 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2002, 09:20:34 ; Search time 14.91 Seconds
(without alignments)
51.557 Million cell updates/sec

Title: US-09-461-061a-1
Perfect score: 45
Sequence: 1 NNATFFFK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 45 | 100.0 | 427 | 1 KGHUL1 | kininogen, LMW pre |
| 2 | 45 | 100.0 | 644 | 1 KGHUL1 | kininogen, HMW pre |
| 3 | 39 | 86.7 | 433 | 2 A28055 | K-kininogen, LMW I |
| 4 | 39 | 86.7 | 639 | 2 A25486 | kininogen, HMW I p |
| 5 | 36 | 80.0 | 858 | 2 T24062 | hypothetical prote |
| 6 | 36 | 80.0 | 1132 | 2 T31107 | telomerase reverse |
| 7 | 35 | 77.8 | 182 | 2 T24206 | hypothetical prote |
| 8 | 34 | 75.6 | 71 | 2 B83803 | hypothetical prote |
| 9 | 34 | 75.6 | 182 | 2 T06978 | ABA-induced plasma |
| 10 | 34 | 75.6 | 273 | 2 F86924 | hypothetical prote |
| 11 | 34 | 75.6 | 319 | 2 A86650 | rhannosyltransfera |
| 12 | 34 | 75.6 | 440 | 2 T11319 | NADH dehydrogenase |
| 13 | 34 | 75.6 | 497 | 2 G96611 | probable cytochrom |
| 14 | 34 | 75.6 | 630 | 2 T25830 | hypothetical prote |
| 15 | 34 | 75.6 | 758 | 2 T31994 | hypothetical prote |
| 16 | 34 | 75.6 | 949 | 2 H97322 | DNA/RNA helicase, |
| 17 | 33 | 73.3 | 303 | 2 T32658 | hypothetical prote |
| 18 | 33 | 73.3 | 332 | 2 T01483 | hypothetical prote |
| 19 | 33 | 73.3 | 469 | 2 F69403 | hypothetical prote |
| 20 | 33 | 73.3 | 603 | 2 S70849 | cholinesterase (EC |
| 21 | 33 | 73.3 | 706 | 2 D84466 | hypothetical prote |
| 22 | 33 | 73.3 | 895 | 2 T23191 | hypothetical prote |
| 23 | 32 | 71.1 | 484 | 2 A40774 | phosphocholine-bin |
| 24 | 32 | 71.1 | 562 | 2 A08052 | secretory protein |
| 25 | 32 | 71.1 | 563 | 2 S54420 | invasion protein i |
| 26 | 32 | 71.1 | 567 | 2 E91095 | type III secretion |
| 27 | 32 | 71.1 | 567 | 2 A85941 | type III secretion |
| 28 | 32 | 71.1 | 606 | 2 T10982 | NADH dehydrogenase |
| 29 | 32 | 71.1 | 1215 | 2 T25078 | hypothetical prote |

| | | | | | |
|----|----|------|------|----------|--------------------|
| 30 | 32 | 71.1 | 1659 | 1 OKBYN2 | protein kinase GCN |
| 31 | 31 | 68.9 | 140 | 2 T10059 | cytokinin-induced |
| 32 | 31 | 68.9 | 148 | 2 B71529 | hypothetical prote |
| 33 | 31 | 68.9 | 171 | 2 F90088 | hypothetical prote |
| 34 | 31 | 68.9 | 190 | 2 F84366 | hypothetical prote |
| 35 | 31 | 68.9 | 196 | 2 F84941 | amidotransferase h |
| 36 | 31 | 68.9 | 202 | 2 AF0604 | probable permease |
| 37 | 31 | 68.9 | 211 | 2 T34501 | hypothetical prote |
| 38 | 31 | 68.9 | 240 | 2 A46179 | U2 snRNP auxiliary |
| 39 | 31 | 68.9 | 249 | 2 F69409 | conserved hypothet |
| 40 | 31 | 68.9 | 262 | 2 S59078 | conserved hypothet |
| 41 | 31 | 68.9 | 264 | 1 JC6125 | U2 small nuclear r |
| 42 | 31 | 68.9 | 334 | 1 RDECEP | N-acetyl-gamma-glu |
| 43 | 31 | 68.9 | 334 | 2 G91239 | N-acetyl-gamma-glu |
| 44 | 31 | 68.9 | 334 | 2 D86087 | N-acetyl-gamma-glu |
| 45 | 31 | 68.9 | 350 | 2 A82299 | outer membrane pro |

ALIGNMENTS

RESULT 1

KGHUL1

kininogen, LMW precursor [validated] - human
N:Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N:Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C:Species: Homo sapiens (man)
C:Date: 06-Jul-1982 #sequence_revision 27-Nov-1985 #text_change 08-Dec-2000
C:Accession: A01280; B25276; A27900; A27699; A31905; A34030
R:Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.
Biochemistry 23, 5691-5697, 1984
A:Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide
A:Reference number: A90490; MUID:85122621
A:Accession: A01280

A:Molecule type: mRNA
A:Residues: 1-427 <OHK>
A:Cross-references: GB:K02566; NID:g177889; PIDN:AAA35497.1; PID:g177890
R:Takagaki, Y.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 8601-8609, 1985
A:Title: Cloning and sequence analysis of cDNAs for human high molecular weight and 1
A:Reference number: A92544; MUID:85234582
A:Accession: B25276

A:Molecule type: mRNA
A:Residues: 1-427 <TAK>
A:Cross-references: GB:M11437; NID:g186751; PIDN:AAB59551.1; PID:g386853
R:Lottspeich, F.; Kellermann, J.; Henschen, A.; Rauth, G.; Mueller-Esterl, W.
in Kinins IV, part A, Greenbaum, L.M., and Margolius, H.S., eds., pp.91-95, Plenum, N
A:Title: Amino acid sequence of the light chain of human low molecular mass kininogen
A:Reference number: A27900
A:Accession: A27900
A:Molecule type: protein
A:Residues: 390-427 <LOT>
R:Mindroul, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A:Title: A new kinin moiety in human plasma kininogens.
A:Reference number: A27699; MUID:88209021
A:Accession: A27699

A:Molecule type: protein
A:Residues: 380-389 <MIN>
R:Maeda, H.; Matsumura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A:Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic f
A:Reference number: A31905; MUID:89034061
A:Accession: A31905
A:Molecule type: protein
A:Residues: 381-389 <MAE>
R:Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A:Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human p
A:Reference number: A34030; MUID:88106632
A:Accession: A34030
A:Molecule type: protein
A:Residues: 380-389 <SAS>

R:Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 260, 8610-8617, 1985
A:Title: Structural organization of the human kininogen gene and a model for its evolution
A:Reference number: A92545; MUID:85234583
A:Contents: annotation; gene organization
R:Pierce, J.V.
Fed. Proc. 27, 52-57, 1968
A:Title: Structural features of plasma kinins and kininogens.
A:Reference number: A91455; MUID:90255622
A:Contents: annotation; bradykinin
C:Comment: The LMW kininogen precursor is produced from the same gene as the HMW form (S)
C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the
C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, and
C:Comment: xiprolin residue is present in the kininogen prior to the release of bradykinin.
C:Genetics:
A:Gene: GDB:KNG
A:Cross-references: GDB:125256; OMIM:228960
A:Map position: 3q27-3q27
A:Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3; 401/3
C:Superfamily: kininogen; cystatin homology
C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glyc
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-427/Product: LMW prokininogen (kininogen I) #status predicted <MAT>
F:19-389-390-427/Product: LMW kininogen II #status predicted <MAT2>
F:19-379/Product: LMW kininogen heavy chain #status predicted <HCH>
F:19-131/Domain: cystatin homology <CX1>
F:142-253/Domain: cystatin homology <CX2>
F:264-375/Domain: cystatin homology <CX3>
F:380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <KB DY>
F:381-389/Product: bradykinin (kallidin I) #status experimental <BDY>
F:390-427/Product: LMW kininogen light chain #status experimental <LCH>
F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:28-407-83-94-107-126-142-145-206-218-229-248-264-267-328-340-351-370/Disulfide bonds:
F:48-169-205-294/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:379-380/Cleavage site: Met-Lys (kallikrein) #status experimental
F:383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F:389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
F:401/Binding site: carbohydrate (Thr) (covalent) #status absent

Query Match 100.0%; Score 45; DB 1; Length 427;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATYFK 8
|||||||
Db 293 NNATYFK 300

RESULT 2
KGUHI
N:Alternate names: alpha-2-thiol proteinase inhibitor; prokininogen; prokininogen
N:Contains: bradykinin (kallidin I); HMW kininogen I; HMW kininogen II; low molecular we
C:Species: Homo sapiens (man)
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 08-Dec-2000
R:Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.
Biochemistry 23, 5691-5697, 1984
A:Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ident
A:Reference number: A90490; MUID:85122621
A:Accession: A01279
A:Molecule type: mRNA
A:Residues: 1-389 <OHK>
A:Cross-references: GB:K02566; NID:g177889
R:Tagakaki, Y.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 8601-8609, 1985
A:Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low
A:Reference number: A92544; MUID:85234582
A:Accession: A25276
A:Molecule type: mRNA
A:Residues: 1-592, 1', 594-644 <TK>
A:Cross-references: GB:M11437; NID:g186751; PIDN:AA859550.1; PID:g386852

R:Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfalg-Machleidt, I.
FEBS Lett. 321, 93-97, 1993
A:Title: Cloning, expression and characterization of human kininogen domain 3.
A:Reference number: S32422; MUID:93223854
A:Accession: S32422
A:Molecule type: mRNA
A:Residues: 'ANSM', 253-377 <AUE>
A:Note: differences are due to known cloning artifacts
R:Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
Eur. J. Biochem. 152, 307-314, 1985
A:Title: The amino acid sequence of the light chain of human high-molecular-mass kini
A:Reference number: A91153; MUID:86030270
A:Accession: A91153
A:Molecule type: protein
A:Residues: 379-644 <LOT>
A:Note: the bradykinin sequence preceding the light chain sequence was not determined
R:Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
Eur. J. Biochem. 154, 471-478, 1986
A:Title: Completion of the primary structure of human high-molecular-mass kininogen.
A:Reference number: A24871; MUID:86108361
A:Accession: A24871
A:Molecule type: protein
A:Residues: 'Z', 20-380 <KEL1>
R:Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
in Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, New
A:Title: Amino acid sequence of the light chain of human high molecular mass kininoge
A:Reference number: A27899
A:Accession: A27899
A:Molecule type: protein
A:Residues: 379-389, 'K', 390-407, 'Q', 409-644 <KEL2>
R:Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A:Title: A new kinin moiety in human plasma kininogens.
A:Reference number: A27699; MUID:98205021
A:Accession: A27699
A:Molecule type: protein
A:Residues: 380-389 <MIN>
R:Maeda, H.; Matsumura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A:Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic f
A:Reference number: A31905; MUID:89034061
A:Accession: A31905
A:Molecule type: protein
A:Residues: 381-389 <MAE>
R:Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A:Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human p
A:Reference number: A34030; MUID:88106632
A:Accession: A34030
A:Molecule type: protein
A:Residues: 380-389 <SAS>
R:Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.
Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A:Title: Human cathepsin B and cysteine proteinase inhibitors (CPis) in inflammatory
A:Reference number: S02482; MUID:89076517
A:Accession: S02482
A:Molecule type: protein
A:Residues: 1-19, 189-192; 310-314; 381-389 <LEN1>
R:Kato, H.; Matsumura, Y.; Maeda, H.
FEBS Lett. 232, 252-254, 1988
A:Title: Isolation and identification of hydroxyproline analogues of bradykinin in hu
A:Reference number: A61495; MUID:88211869
A:Accession: A61495
A:Molecule type: protein
A:Residues: 380-389 <KAT1>
A:Experimental source: urine
A:Note: this peptide had Pro-383 modified to 4-hydroxyproline
A:Accession: B61495
A:Molecule type: protein
A:Residues: 381-389 <KAT2>
A:Experimental source: urine
A:Note: this peptide had Pro-383 modified to 4-hydroxyproline
A:Accession: C61495

A:Molecule type: protein
A:Residues: 380-389 <KAT3>
R:Lenarcic, B.; Krasovec, M.; Ritonja, A.; Olafsson, I.; Turk, V.
FEBS Lett. 280, 211-215, 1991
A:Title: Inactivation of human cystatin C and kininogen by human cathepsin D.
A:Reference number: S14303; MUID:91192133
A:Accession: S14447
A:Molecule type: protein
A:Residues: 264-359, 'N', 361-375 <LEN2>
R:Little, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A:Title: Human mast cell tryptase isoforms: separation and examination of substrate-specificity
A:Reference number: S55239; MUID:95251593
A:Accession: S55239
A:Molecule type: protein
A:Residues: 450-452, 'X', 454, 'X', 456 <LIT>
R:Straczek, J.; Maechli, F.; le Nguyen, D.; Becchi, M.; Heulin, M.H.; Nabet, P.; Belleville, J.
FEBS Lett. 373, 207-211, 1995
A:Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like growth factor release
A:Reference number: S68059; MUID:96033974
A:Accession: S68059
A:Molecule type: protein
A:Residues: 431-434 <STR>
R:Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 260, 8610-8617, 1985
A:Title: Structural organization of the human kininogen gene and a model for its evolution
A:Reference number: A92545; MUID:85234583
A:Accession: A92545
A:Contents: annotation; gene organization
R:Pierce, J.V., 52-57, 1968
Fed. Proc. 27, 52-57, 1968
A:Title: Structural features of plasma kinins and kininogens.
A:Reference number: A91455; MUID:90255622
A:Accession: A91455
A:Contents: annotation; bradykinin
C:Comment: The HMW kininogen precursor and the LMW form are produced from the same gene.
C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the blood coagulation cascade.
C:Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is implicated in the release of bradykinin.
C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, and its release is regulated by the presence of the kininogen prior to the release of bradykinin.
C:Genetics:
A:Gene: GDB:KNG
A:Cross-references: GDB:125256; OMIM:228960
A:Map position: 3q27-3q28
A:Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
A:Superfamily: Kininogen; cystatin homology
C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; duplication
F:1-18/Domain: signal sequence #status experimental <SIG>
F:19-644/Product: HMW kininogen I (prokininogen) #status experimental <MAT1>
F:19-379, 390-644/Product: HMW kininogen II #status experimental <MAT2>
F:19-379/Domain: HMW kininogen heavy chain #status experimental <HCH>
F:19-131/Domain: cystatin homology <CY1>
F:142-253/Domain: cystatin homology <CY2>
F:264-375/Domain: cystatin homology <CY3>
F:380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F:381-389/Product: bradykinin (kallidin I) #status experimental <BDY>
F:390-644/Domain: HMW kininogen light chain #status experimental <LCH>
F:421-510/Region: glycine/histidine/lysine-rich 30-residue repeats
F:431-434/Product: low molecular weight growth promoting factor #status experimental <GF>
F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental <G19>
F:28-614, 83-94, 107-126, 142-145, 206-218, 229-248, 264-267, 328-340, 351-370/Disulfide bonds:
F:48/Binding site: carboxylate (Asn) (covalent) #status experimental
F:169, 205, 294/Binding site: carboxylate (Asn) (covalent) #status experimental
F:379-380/Cleavage site: Met-Lys (kallikrein) #status experimental
F:383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F:389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
F:401, 533, 542, 546, 557, 571, 593, 628/Binding site: carboxylate (Thr) (covalent) #status experimental
F:577/Binding site: carboxylate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 45; DB 1; Length 644;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFEYFK 8

Db 293 NNATFEYFK 300

RESULT 3
A28055

K:kininogen, LMW I precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
C:Accession: A28055
R:Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A:Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin a and b.
A:Reference number: A92496; MUID:86008264
A:Accession: A28055
A:Molecule type: mRNA
A:Residues: 1-433 <FUR>
C:Superfamily: Kininogen; cystatin homology
C:Keywords: alternative splicing
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-433/Product: k-kininogen, LMW I #status predicted <MAT>
F:19-131/Domain: cystatin homology <CY1>
F:142-253/Domain: cystatin homology <CY2>
F:264-375/Domain: cystatin homology <CY3>

Query Match 86.7%; Score 39; DB 2; Length 433;
Best Local Similarity 87.5%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFEYFK 8

Db 293 NNATFEYFK 300

RESULT 4
A25486

N:kininogen, HMW I precursor - rat
N:Contains: bradykinin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
C:Accession: A25486
R:Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A:Title: Differing expression patterns and evolution of the rat kininogen gene family
A:Reference number: A92625; MUID:87137443
A:Accession: A25486
A:Molecule type: mRNA
A:Residues: 1-639 <KIT>
A:Note: the authors translated the codon CAA for residue 347 as Asn
C:Superfamily: Kininogen; cystatin homology
C:Keywords: alternative splicing
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-639/Product: kininogen, HMW I #status predicted <MAT>
F:19-131/Domain: cystatin homology <CY1>
F:142-253/Domain: cystatin homology <CY2>
F:264-375/Domain: cystatin homology <CY3>

Query Match 86.7%; Score 39; DB 2; Length 639;
Best Local Similarity 87.5%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFEYFK 8

Db 293 NNATFEYFK 300

RESULT 5
T24062

C:Species: Caenorhabditis elegans
hypothetical protein R09A8.2 - Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T24062
R:Wilkinson, J.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19836
A:Accession: T24062
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-858 <WIL>
A:Cross-references: EMBL:Z68009; PIDN:CAA92004.1; GSPDB:GNO0028; CESP:R09A8.2
A:Experimental source: clone R09A8
C:Genetics:
A:Gene: CESP:R09A8.2
A:Map position: X
A:Introns: 197/1; 324/3; 377/3; 435/3; 495/3; 587/1; 627/3; 730/3; 812/1

Query Match 80.0%; Score 36; DB 2; Length 858;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
| :|||||
Db 49 NESTFYFK 56

RESULT 6
T31107
telomerase reverse transcriptase - Oxytricha trifallax
C:Species: Oxytricha trifallax
C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C:Accession: T31107
R:Bryan, T.M.; Sperger, J.M.; Chapman, K.B.; Cech, T.R.
Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998
A:Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytricha
A:Reference number: Z20985; MUID:98337940
A:Accession: T31107
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1132 <BRY>
A:Cross-references: EMBL:AF060230; NID:g3342795; PID:g3342796; PIDN:AAC39163.1
C:Genetics:
A:Gene: TERT

Query Match 80.0%; Score 36; DB 2; Length 1132;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
| :|||||
Db 1001 NNISFYFK 1008

RESULT 7
T24206
hypothetical protein R12H7.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Dec-2000
C:Accession: T24206
R:Coles, L.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z19854
A:Accession: T24206
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-182 <WIL>
A:Cross-references: EMBL:Z50755; PIDN:CAA90635.1; GSPDB:GNO0028; CESP:R12H7.3
A:Experimental source: clone R12H7
C:Genetics:
A:Gene: CESP:R12H7.3
A:Map position: X
A:Introns: 150/3

C:Superfamily: human S-phase kinase-associated protein 1A

Query Match 77.8%; Score 35; DB 2; Length 182;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
| :|||||
Db 161 NNATLFFK 168

RESULT 8
B83803
hypothetical protein BH1226 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: B83803
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B83803
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <STO>
A:Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BA04945.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1226

Query Match 75.6%; Score 34; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATFYF 7
| :|||||
Db 43 NATFYF 48

RESULT 9
T06978
ABA-induced plasma membrane protein PM 19 - wheat
C:Species: Triticum aestivum (common wheat)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
C:Accession: T06978
R:Koike, M.; Takezawa, D.; Arakawa, K.; Yoshida, S.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z15842
A:Accession: T06978
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-182 <KOI>
A:Cross-references: EMBL:U80037; NID:g1724111; PIDN:AAB38504.1; PID:g1724112
A:Experimental source: cv. Chihoku
C:Genetics:
A:Note: WTABAPM

Query Match 75.6%; Score 34; DB 2; Length 182;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFYF 7
| :|||||
Db 47 NGATFYF 53

RESULT 10
F86924
hypothetical protein [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae

Query Match 75.6%; Score 34; DB 2; Length 630;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 NNATFYFK 8
: || ||||
Db 444 SNAQFYFK 451

RESULT 15

T31994
hypothetical protein C49D10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31994
R:Henkhaus, J.; Wohlmann, P.; Beck, C.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid C49D10.
A:Reference number: Z21108
A:Accession: T31994
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-758 <HEN>
A:Cross-references: EMBL:AF016665; PIDN:AACT1186.1; GSPDB:GN00020; CESP:C49D10.1
A:Experimental source: strain Bristol N2; clone C49D10
C:Genetics:
A:Gene: CESP:C49D10.1
A:Map position: 2
A:Introns: 438/2

Query Match 75.6%; Score 34; DB 2; Length 758;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 NNATFYFK 8
: || ||||
Db 598 SNAQFYFK 605

Search completed: July 10, 2002, 09:21:18
Job time: 44 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2002, 09:20:34 ; Search time 10.34 Seconds
(without alignments)
29.957 Million cell updates/sec

Title: US-09-461-061A-1
Perfect score: 45
Sequence: 1 NNATFYFK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|--------------|--------------------|
| 1 | 45 | 100.0 | 644 | 1 KNG_HUMAN | P01042 homo sapien |
| 2 | 39 | 86.7 | 639 | 1 KNG_RAT | P08934 rattus norv |
| 3 | 36 | 80.0 | 1132 | 1 TERT_OXYTR | Q07632 oxytricha t |
| 4 | 33 | 73.3 | 603 | 1 CHLE_MOUSE | Q03311 mus musculu |
| 5 | 32 | 71.1 | 562 | 1 INVG_SALTY | P35672 salmonella |
| 6 | 32 | 71.1 | 1590 | 1 GCN2_YEAST | P15442 saccharomyc |
| 7 | 31 | 68.9 | 82 | 1 U2AG_PIG | Q29350 sus scrofa |
| 8 | 31 | 68.9 | 196 | 1 HIS5_BUCAI | P57204 buchnera ap |
| 9 | 31 | 68.9 | 239 | 1 U2AG_MOUSE | Q9d883 mus musculu |
| 10 | 31 | 68.9 | 239 | 1 U2AG_HUMAN | Q01081 homo sapien |
| 11 | 31 | 68.9 | 264 | 1 U2AG_DROME | Q94535 drosophila |
| 12 | 31 | 68.9 | 334 | 1 ARGC_ECOLI | P11446 escherichia |
| 13 | 31 | 68.9 | 341 | 1 OMPU_VIBCH | P97085 vibrio chol |
| 14 | 31 | 68.9 | 434 | 1 KNL2_BOVIN | P01047 bos taurus |
| 15 | 31 | 68.9 | 441 | 1 PAFA_HUMAN | Q13093 h platelet- |
| 16 | 31 | 68.9 | 444 | 1 PAFA_CANFA | Q28262 c platelet- |
| 17 | 31 | 68.9 | 619 | 1 KNH2_BOVIN | P01045 bos taurus |
| 18 | 31 | 68.9 | 623 | 1 RSD1_YEAST | P32368 saccharomyc |
| 19 | 31 | 68.9 | 901 | 1 VEF_GVPU | P41723 pseudolatia |
| 20 | 31 | 68.9 | 901 | 1 VEF_GVTN | P29998 trichoplusi |
| 21 | 31 | 68.9 | 902 | 1 VEF_GVHA | P54232 heliothis a |
| 22 | 31 | 68.9 | 988 | 1 ST23_YEAST | Q06010 saccharomyc |
| 23 | 31 | 68.9 | 1066 | 1 NUC2_NEUCR | Q01317 neurospora |
| 24 | 31 | 68.9 | 2710 | 1 TOXA_CLODI | P16154 clostidium |
| 25 | 31 | 68.9 | 4725 | 1 DYHC_DICDI | P34036 dictyostell |
| 26 | 30 | 66.7 | 163 | 1 SFAS_ECOLI | P13430 escherichia |
| 27 | 30 | 66.7 | 196 | 1 HIS5_METJA | Q57929 methanococc |
| 28 | 30 | 66.7 | 208 | 1 LEUD_BUCDN | Q85073 buchnera ap |
| 29 | 30 | 66.7 | 237 | 1 YS76_CAEEL | Q09619 caenorhabdi |
| 30 | 30 | 66.7 | 259 | 1 KKA6_ACIBA | P09885 acinetobact |
| 31 | 30 | 66.7 | 331 | 1 NIXA_HELPJ | Q9zm74 helicobacte |
| 32 | 30 | 66.7 | 331 | 1 NIXA_HELPY | Q48262 helicobacte |
| 33 | 30 | 66.7 | 365 | 1 NMPC_ECOLI | P21420 escherichia |

RESULT 1

| ID | KNG_HUMAN | STANDARD; | PRT; | 644 AA. |
|----|---|-----------|------|---------|
| AC | P01042; P01043; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 01-FEB-1996 (Rel. 33, Last sequence update) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) | | | |
| DE | Kininogen precursor (Alpha-2-thiol proteinase inhibitor) [Contains: Bradykinin]. | | | |
| DE | KNG. | | | |
| GN | Homo sapiens (Human). | | | |
| OS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW). | | | |
| RC | TISSUE=Liver; PubMed-2989293; | | | |
| RX | MEDLINE=85234582; PubMed-2989293; | | | |
| RA | Takagaki Y., Kitamura N., Nakanishi S.; | | | |
| RT | "Cloning and sequence analysis of cDNAs for human high molecular weight and low molecular weight prekininogens. Primary structures of two human prekininogens." | | | |
| RT | J. Biol. Chem. 260:8601-8609(1985). | | | |
| RN | [2] | | | |
| RP | GENE STRUCTURE. | | | |
| RX | MEDLINE=85234583; PubMed-2989294; | | | |
| RA | Kitamura N., Kitagawa H., Fukushima D., Takagaki Y., Miyata T., Nakanishi S.; | | | |
| RT | "Structural organization of the human kininogen gene and a model for its evolution." | | | |
| RT | J. Biol. Chem. 260:8610-8617(1985). | | | |
| RN | [3] | | | |
| RP | SEQUENCE OF 1-401 FROM N.A. | | | |
| RX | MEDLINE=85122621; PubMed-6441591; | | | |
| RA | Ohkubo I., Kurachi K., Takasawa T., Shiokawa H., Sasaki M.; | | | |
| RT | "Isolation of a human cDNA for alpha 2-thiol proteinase inhibitor and its identity with low molecular weight kininogen." | | | |
| RL | Biochemistry 23:5691-5697(1984). | | | |
| RN | [4] | | | |
| RP | SEQUENCE OF 379-644. | | | |
| RX | MEDLINE=86030270; PubMed-4054110; | | | |
| RA | Lottspeich F., Kellermann J., Foertsch B., Mueller-Esterl W.; | | | |
| RT | "The amino acid sequence of the light chain of human high-molecular-mass kininogen." | | | |
| RT | Eur. J. Biochem. 152:307-314(1985). | | | |
| RN | [5] | | | |
| RP | SEQUENCE OF 381-389. | | | |
| RX | MEDLINE=90255622; PubMed-4952632; | | | |
| RA | Pierce J.V.; | | | |
| RT | "Structural features of plasma kinins and kininogens." | | | |
| RL | Red. Proc. 27:52-57(1968). | | | |
| RN | [6] | | | |
| RP | DISULFIDE BONDS. | | | |
| RA | Sueyoshi T., Miyata T., Kato H., Iwanaga S.; | | | |
| RT | "Disulfide bonds in bovine HMW kininogens." | | | |

P34845 apis mellif
Q09919 schizosacch
P38128 saccharomyc
Q97855 streptococc
O55071 mus musculu
P40583 saccharomyc
P09289 varicella-z
P21927 oryctolagus
P06276 homo sapien
O63908 myoxus glis
Q24371 drosophila
Q92882 chlamydia p

RL Mol. Microbiol. 13:555-568(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE-21534948; PubMed-11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 CC -!- FUNCTION: INVOLVED IN THE INVASION OF THE CELLS OF THE INTESTINAL
 CC EPITHELIUM. COULD BE NECESSARY FOR THE EXPORT OF INVASION RELATED
 CC DETERMINANTS.
 CC -!- SUBCELLULAR LOCATION: Outer membrane (Potential).
 CC -!- SIMILARITY: BELONGS TO THE PULD/OUTD/EXED/XPSD FAMILY.
 CC -----
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 DR EMBL; X75302; CAAS3049.1; -;
 DR EMBL; U08280; AAA74040.1; -;
 DR EMBL; AE008832; AAL21778.1; -;
 DR PIR; S38422; S38422.
 DR StyGene; SG10188; invG.
 DR InterPro; IPR000016; Bac-GSPproteins.
 DR PRINTS; PR01337; TYPE3OMGPROT.
 DR PROSITE; PS00875; T2SP.D; 1.
 KW Virulence; Transport; Protein transport; Signal; Outer membrane;
 KW Complete proteome.
 FT SIGNAL 1 14 POTENTIAL.
 FT CHAIN 15 562 INV G PROTEIN.
 FT CONFLICT 12 12 A -> R (IN REF. 2).
 FT CONFLICT 121 121 E -> Q (IN REF. 2).
 FT CONFLICT 197 205 LRQKQVVP -> CAIRKWLFR (IN REF. 2).
 FT CONFLICT 232 240 AMPAFSANG -> RCQRFQM (IN REF. 2).
 FT CONFLICT 243 243 G -> S (IN REF. 2).
 FT CONFLICT 262 264 AAA -> KPAEQ (IN REF. 2).
 FT CONFLICT 328 328 S -> T (IN REF. 1 AND 2).
 FT CONFLICT 329 329 I -> V (IN REF. 2).
 FT CONFLICT 370 380 RPLVLTQENVP -> APTGTSKGCS (IN REF. 2).
 SQ SEQUENCE 562 AA; 61765 MW; 8022905BE256058D CRC64;

 QY 1 NNATFFFK 8
 DB 385 NNATFFTK 392

 RESULT 6
 GCN2_YEAST
 ID GCN2_YEAST STANDARD; PRT; 1590 AA.
 AC P15442;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Protein kinase GCN2 (EC 2.7.1.-).
 GN GCN2 OR AAS1 OR YDR283C.
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; *Saccharomycotina*; *Saccharomycetes*;

OC Saccharomycetales; *Saccharomycetaceae*; *Saccharomyces*.
 OX NCBI_taxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-89282814; PubMed-2660141;
 RX MEDLINE-89282814; PubMed-2660141;
 RA Wek R.C., Jackson B.M., Hinnebusch A.G.;
 RT "Juxtaposition of domains homologous to protein kinases and histidyl-
 RT tRNA synthetases in GCN2 protein suggests a mechanism for coupling
 RT GCN4 expression to amino acid availability.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4579-4583(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RX MEDLINE-88261291; PubMed-3290651;
 RA Roussou I., Thireos G., Hauge B.M.;
 RT "Transcriptional-translational regulatory circuit in *Saccharomyces*
 RT *cerevisiae* which involves the GCN4 transcriptional activator and the
 RT GCN2 protein kinase.";
 RL Mol. Cell. Biol. 8:2132-2139(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RA Le T.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP ASSOCIATION WITH RIBOSOMES.
 RX MEDLINE-91246169; PubMed-2038314;
 RA Ramirez M., Wek R.C., Hinnebusch A.G.;
 RT "Ribosome association of GCN2 protein kinase, a translational
 RT activator of the GCN4 gene of *Saccharomyces cerevisiae*.";
 RL Mol. Cell. Biol. 11:3027-3036(1991).
 RN [5]
 RP ACTIVITY ON SUI2.
 RX MEDLINE-92154672; PubMed-1739968;
 RA Dever T.E., Feng L., Wek R.C., Cigan A.M., Donahue T.D.,
 RA Hinnebusch A.G.;
 RT "Phosphorylation of initiation factor 2 alpha by protein kinase GCN2
 RT mediates gene-specific translational control of GCN4 in yeast.";
 RL Cell 68:585-596(1992).
 CC -!- FUNCTION: STIMULATES GCN4 TRANSLATION IN AMINO ACID-STARVED CELLS
 CC BY PHOSPHORYLATING THE ALPHA SUBUNIT OF EIF-2 (SUI2) ON SER-52.
 CC -!- SUBCELLULAR LOCATION: ASSOCIATES WITH THE 60S SUBUNIT OF
 CC RIBOSOMES.
 CC -!- INDUCTION: BY AMINO ACID STARVATION AND IN THE PRESENCE OF THE
 CC GCN4 PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC GCN2 SUBFAMILY.
 CC -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 301
 CC TO 364 AND FROM POSITION 981 ONWARD DUE TO FRAMESHIFTS.
 CC -----
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 CC -----
 DR EMBL; M27082; AAA34636.1; -;
 DR EMBL; M20487; AAA34881.1; ALT_FRAME.
 DR EMBL; U51030; AAB64461.1; ALT_INIT.
 DR PIR; S05781; OKBYN2.
 DR PIR; A27723; A27723.
 DR HSP; P24941; IJST.
 DR SGD; S0002691; GCN2.
 DR InterPro; IPR002106; AA_trna_ligase_II.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; pkinase; 4.
 DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.

KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Amino-acid biosynthesis; Aminoacyl-tRNA synthetase; Repeat.
FT DOMAIN 187 458 PROTEIN KINASE 1.
FT DOMAIN 530 912 PROTEIN KINASE 2.
FT DOMAIN 930 1450 HISTIDYL-TRNA SYNTHETASE LIKE.
FT NP_BIND 536 544 ATP (BY SIMILARITY).
FT BINDING 559 559 ATP (BY SIMILARITY).
FT ACT_SITE 766 766 TIKAKLP -> NYKQKIA (IN REF. 2).
FT CONFLICT 151 157 LMSSEMEN -> YVFSNKGKS (IN REF. 2).
FT CONFLICT 202 210 I -> M (IN REF. 2).
FT CONFLICT 406 406 P -> A (IN REF. 2).
FT CONFLICT 520 520 RSRVADFEETAVL -> DHDMLTLRLHFS
FT CONFLICT 523 536 (IN REF. 2).
FT CONFLICT 553 553 S -> T (IN REF. 2).
FT CONFLICT 571 572 IL -> MI (IN REF. 2).
FT CONFLICT 658 658 F -> C (IN REF. 2).
FT CONFLICT 770 770 M -> K (IN REF. 2).
FT CONFLICT 885 885 E -> Q (IN REF. 2).
SQ SEQUENCE 1590 AA; 182041 MW; 768815424F64F1AA CRC64;

Query Match 71.18; Score 32; DB 1; Length 1590;
Best Local Similarity 75.08; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8

|||||:

Db 266 NNATFVWK 273

RESULT 7

ID U2AG_PIG STANDARD; PRT; 82 AA.
AC Q29350;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Splicing factor U2AF 35 kDa subunit (U2 auxiliary factor 35 kDa
DE subunit) (U2 snRNP auxiliary factor small subunit) (Fragment).
GN U2AF1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96327607; PubMed=8672129;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library: analysis of 839 clones.";
RL Mamm. Genome 7:509-517(1996).
CC -1- FUNCTION: PLAYS A CRITICAL ROLE IN BOTH CONSTITUTIVE AND ENHANCER-
CC DEPENDENT SPLICING BY MEDIATING ESSENTIAL PROTEIN-PROTEIN
CC INTERACTIONS AND PROTEIN-RNA INTERACTIONS REQUIRED FOR ACCURATE 3'
CC SPLICE SITE SELECTION. DIRECTLY MEDIATES INTERACTIONS BETWEEN
CC U2AF65 (LARGE SUBUNIT) AND PROTEINS BOUND TO THE ENHANCERS AND
CC THIS MAY FUNCTION AS A BRIDGE BETWEEN U2AF65 AND THE ENHANCER
CC COMPLEX TO RECRUIT IT TO THE ADJACENT INTRON (BY SIMILARITY).
CC -1- SUBUNIT: ASSOCIATES WITH A 65 KDa PROTEIN.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
CC -1- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
CC
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DR EMBL; F14757; CAA23231.1; -.
DR InterPro; IPR000571; zf-CCCH.
DR Pfam; PF00642; zf-CCCH; 1.
KW Nuclear protein; RNA-binding; mRNA splicing; Zinc-finger; Repeat.
FT DOMAIN 47 >82 INVOLVED IN BINDING U2AF-65 (BY
FT SIMILARITY).
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9416 MW; 96882458044823A8 CRC64;

Query Match 68.98; Score 31; DB 1; Length 82;
Best Local Similarity 71.48; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NATFYFK 8

|||||

Db 17 NCSFYFK 23

RESULT 8

ID HIS5_BUCAI STANDARD; PRT; 196 AA.
AC P57204;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Amidotransferase hish (EC 2.4.2.-).
GN HISH OR BUL03.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OC symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOKYO 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: CATALYZES AN AMIDOTRANSFERASE REACTION THAT GENERATES
CC IMIDAZOLE-GLYCEROL PHOSPHATE AND 5-AMINOIMIDAZOL-4-CARBOXYAMIDE
CC RIBONUCLEOTIDE, WHICH IS USED FOR PURINE SYNTHESIS.
CC -1- PATHWAY: FIFTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: BELONGS TO THE HISH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.

CC
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DR EMBL; AP001118; BAB12822.1; -.

DR InterPro; IPR000991; GATase_1.

DR Pfam; PF00117; GATase; 1.

DR PROSITE; PS00442; GATASE_TYPE_I; FALSE_NEG.

KW Histidine biosynthesis; Transferase; Glutamine amidotransferase;

KW Complete proteome.

FT ACT_SITE 77 77 BY SIMILARITY.

FT ACT_SITE 178 178 BY SIMILARITY.

FT ACT_SITE 180 180 BY SIMILARITY.

SQ SEQUENCE 196 AA; 21679 MW; 904624B74BBE5D CRC64;

Query Match 68.98; Score 31; DB 1; Length 196;
Best Local Similarity 71.48; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFYF 7

Db 135 NNSRFFYF 141

RESULT 9

U2AG_MOUSE

ID U2AG_MOUSE STANDARD; PRT; 239 AA.
AC Q9D883; Q9CZ98; Q99LX2;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Splicing factor U2AF 35 kDa subunit (U2 auxiliary factor 35 kDa
DE subunit) (U2 snRNP auxiliary factor small subunit).
OS U2AF1.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE OF 2-239 FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PLAYS A CRITICAL ROLE IN BOTH CONSTITUTIVE AND ENHANCER-
CC DEPENDENT SPLICING BY MEDIATING ESSENTIAL PROTEIN-PROTEIN
CC INTERACTIONS AND PROTEIN-RNA INTERACTIONS REQUIRED FOR ACCURATE 3'
CC SPLICING SITE SELECTION. DIRECTLY MEDIATES INTERACTIONS BETWEEN
CC U2AF65 (LARGE SUBUNIT) AND PROTEINS BOUND TO THE ENHANCER AND
CC THIS MAY FUNCTION AS A BRIDGE BETWEEN U2AF65 AND THE ENHANCER
CC COMPLEX TO RECRUIT IT TO THE ADJACENT INTRON (By similarity).
CC -!- SUBUNIT: ASSOCIATES WITH A 65 kDa PROTEIN (By similarity).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (By similarity).
CC -!- DOMAIN: THE AMINO-TERMINAL SR-RICH DOMAIN IS REQUIRED FOR
CC INTERACTIONS WITH SR PROTEINS AND THE SPLICING REGULATORS TRA AND
CC TRA2, AND THE CARBOXY-TERMINAL DOMAIN IS REQUIRED FOR FORMATION OF
CC THE U2AF35/U2AF65 HETERODIMER (By similarity).
CC -!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
CC -!- SIMILARITY: CONTAINS 2 C3H1-TYPE ZINC FINGERS.
CC -!- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
CC
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CC
CC EMBL; AK008332; BAB25609.1; -

DR EMBL; AK012849; BAB28511.1; -
DR EMBL; BC002184; AAH02184.1; -
DR MGD; MGI:98884; U2af1.
DR InterPro; IPR000504; RRM.
DR InterPro; IPR003954; RRM_1.
DR InterPro; IPR000571; Zf-CCCH.
DR Pfam; PF00076; rrm; 1.
DR Pfam; PF0642; zf-CCCH; 2.
DR SMART; SM00360; RRM; 1.
DR SMART; SM00361; RRM_1; 1.
DR SMART; SM00356; Znf_C3H1; 2.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS00303; RRM_RNP_1; FALSE NEG.
KW Nuclear protein; RNA-binding; mRNA splicing; Zinc-finger; Repeat.
FT ZN_FING 13 41 C3H1-TYPE 1
FT DOMAIN 65 147 RNA-BINDING (RRM).
FT ZN_FING 149 173 C3H1-TYPE 2.
FT DOMAIN 179 238 ARG/GLY/SER-RICH (RS DOMAIN).
FT CONFLICT 187 187 G -> R (IN REF. 1; BAB25609).
SQ SEQUENCE 239 AA; 27815 MW; DFF944210581244D CRC64;

Query Match 68.9%; Score 31; DB 1; Length 239;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NATFYFK 8

DB 17 NCSFYFK 23

RESULT 10

U2AG_HUMAN

ID U2AG_HUMAN STANDARD; PRT; 240 AA.
AC Q01081;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Splicing factor U2AF 35 kDa subunit (U2 auxiliary factor 35 kDa
DE subunit) (U2 snRNP auxiliary factor small subunit).
GN U2AF1 OR U2AF35.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 68-89 AND 126-151.
RC TISSUE=Fetal brain;
RX MEDLINE=92409598; PubMed=1388271;
RA Zhang M., Zamore P.D., Carmo-Fonseca M., Lamond A.I., Green M.R.;
RT "Cloning and intracellular localization of the U2 small nuclear
RT ribonucleoprotein auxiliary factor small subunit";
RL Proc. Natl. Acad. Sci. U.S.A. 89:8769-8773(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordiek G., Hornischer K., Brandt P.,
RA Schaefer M., Schoen A., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramer J., Beck A., Klages S., Hennig S., Riessmann L., Dagand E.,
RA Wehmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Vaspo M.-L.;
RT "The DNA sequence of human chromosome 21";
RL Nature 405:311-319(2000).
RN [3]
RP FUNCTION.
RX MEDLINE=96249383; PubMed=8647433;

RA Zuo P., Maniatis T.;
RT "The splicing factor U2AF35 mediates critical protein-protein
RL interactions in constitutive and enhancer-dependent splicing."
RL Genes Dev. 10:1356-1368(1996).
CC -!- FUNCTION: PLAYS A CRITICAL ROLE IN BOTH CONSTITUTIVE AND ENHANCER-
CC DEPENDENT SPLICING BY MEDIATING ESSENTIAL PROTEIN-PROTEIN
CC INTERACTIONS AND PROTEIN-RNA INTERACTIONS REQUIRED FOR ACCURATE 3'
CC SPLICE SITE SELECTION. DIRECTLY MEDIATES INTERACTIONS BETWEEN
CC U2AF65 (LARGE SUBUNIT) AND PROTEINS BOUND TO THE ENHANCERS AND
CC U2AF35 (SMALL SUBUNIT) AS A BRIDGE BETWEEN U2AF65 AND THE ENHANCER
CC COMPLEX TO RECRUIT IT TO THE ADJACENT INTRON.
CC -!- SUBUNIT: ASSOCIATES WITH A 65 kDa PROTEIN.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: THE AMINO-TERMINAL SR-RICH DOMAIN IS REQUIRED FOR
CC INTERACTIONS WITH SR PROTEINS AND THE SPLICING REGULATORS TRA AND
CC TRA2, AND THE CARBOXY-TERMINAL DOMAIN IS REQUIRED FOR FORMATION OF
CC THE U2AF35/U2AF65 HETERODIMER.
CC -!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
CC -!- SIMILARITY: CONTAINS 2 C3H1-TYPE ZINC FINGERS.
CC -!- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
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CC -----
DR EMBL; M96982; AAA36619.1; -;
DR EMBL; AP001748; BAA95534.1; -;
DR PIR; S27969; S27969.
DR PIR; A46179; A46179.
DR MIM; 191317; -;
DR InterPro; IPR000504; RRM.
DR InterPro; IPR000571; Zf-CCCH.
DR Pfam; PF00076; rrm; 1.
DR Pfam; PF00642; zf-CCCH; 2.
DR SMART; SM00360; RRM; 1.
DR SMART; SM00356; Znf-C3H1; 2.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
KW Nuclear protein; RNA-binding; mRNA splicing; zinc-finger; Repeat.
FT ZN_FING 13 41
FT DOMAIN 65 147
FT ZN_FING 149 173
FT DOMAIN 178 240
FT ZN_FING 210 223
FT DOMAIN 210 223
SQ SEQUENCE 240 AA; 27872 MW; 3DA130DCE0B953F6 CRC64;
Query Match 68.9%; Score 31; DB 1; Length 240;
Best Local Similarity 71.4%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 NATFFYK 8
Db 17 NCSFYFK 23
RESULT 11
U2AG_DROME STANDARD; PRT; 264 AA.
AC Q94535; Q9VFN4;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Splicing factor U2af 38 kDa subunit (U2 auxiliary factor 38 kDa
DE subunit) (U2 SNRNP auxiliary factor small subunit).
GN U2AF38 OR CG3582.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=96413646; PubMed=8816800;
RA Rudner D.Z., Kanaar R., Breger K.S., Rio D.C.;
RT "Mutations in the small subunit of the Drosophila U2AF splicing
RT factor cause lethality and developmental defects";
RL proc. Natl. Acad. Sci. U.S.A. 93:10333-10337(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Richards S.D., Zhang Q., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: NECESSARY FOR THE SPLICING OF PRE-MRNA. BINDS TO THE
CC POLYPYRIMIDINE TRACT OF INTRONS EARLY DURING SPLICESOME ASSEMBLY
CC (BY SIMILARITY).
CC -!- SUBUNIT: ASSOCIATES WITH A 65 kDa PROTEIN (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
CC -!- SIMILARITY: CONTAINS 2 C3H1-TYPE ZINC FINGERS.
CC -!- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
CC -----
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CC -----
DR EMBL; U67066; AAB17271.1; -;
DR EMBL; AE003590; AAP51512.1; -;
DR FlyBase; FBgn0017457; U2af38.
DR InterPro; IPR000504; RRM.

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DR InterPro: IPR003954; RRM_1.
DR InterPro: IPR000571; Zf-CCCH.
DR Pfam: PF00076; rrm; 1.
DR Pfam: PF00842; zf-CCCH; 2.
DR SMART: SM00361; RRM_1; 1.
DR SMART: SM00356; Znf_C3H1; 2.
DR PROSITE: PS0102; RRM; 1.
DR PROSITE: PS00030; RRM_RNP_1; FALSE_NEG.
KW Nuclear protein; RNA-binding; mRNA splicing; Zinc-finger; Repeat.
FT DOMAIN 44 149 RNA-BINDING (RRM).
FT DOMAIN 180 213 ARG/SER-RICH (RS DOMAIN).
FT DOMAIN 190 197 POLY-ARG.
FT DOMAIN 252 262 POLY-GLY.
FT CONFLICT 66 66 H -> D (IN REF. 1).
SQ SEQUENCE 264 AA; 29877 MW; 577285FB66FDB2F5 CRC64;

Query Match 68.9%; Score 31; DB 1; Length 264;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NATFYFK 8
DB 17 NCSFYFK 23

RESULT 12
ARGC_ECOLI STANDARD; PRT; 334 AA.
AC P11446;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-
DE acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
GN ARGC OR B3958.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89121510; PubMed=2851495;
RA Parsot C., Boyen A., Cohen G.N., Glandsdorff N.;
RT "Nucleotide sequence of Escherichia coli argB and argC genes:
RT Comparison of N-acetylglutamate kinase and
RT N-acetylglutamate-gamma-semialdehyde dehydrogenase with homologous
RT and analogous enzymes.";
RL Gene 68:275-283(1988).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=94089392; PubMed=8265357;
RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA Daniels D.L.;
RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
RT region from 89.2 to 92.8 minutes.";
RL Nucleic Acids Res. 21:5408-5417(1993).
[3]
RP SEQUENCE OF 1-48 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=83143275; PubMed=6761650;
RA Piette J., Cunin R., Boyen A., Charlier D.R.M., Crabeel M.,
RA van Vliet F., Glandsdorff N., Squires C., Squires C.L.;
RT "The regulatory region of the divergent argECBH operon in Escherichia
RT coli K-12.";
RL Nucleic Acids Res. 10:8031-8048(1982).
[4]
RP SEQUENCE OF 1-19 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92202162; PubMed=1551850;
RA Meinel T., Schmitt E., Mechulam Y., Blanquet S.;
RT "Structural and biochemical characterization of the Escherichia coli

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RT argE gene product.";
RL J. Bacteriol. 174:2323-2331(1992).
CC -|- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+)
CC + phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
CC -|- PATHWAY: THIRD STEP IN ARGININE BIOSYNTHESIS.
CC -|- SIMILARITY: BELONGS TO THE NAGSA DEHYDROGENASE FAMILY.
CC -----
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CC -----
DR EMBL; M21446; AAA23477.1; -.
DR EMBL; J01587; AAB59146.1; -.
DR EMBL; X55417; -; NOT_ANNOTATED_CDS.
DR EMBL; U00006; AAC43064.1; -.
DR EMBL; AE000470; AAC76940.1; -.
DR PIR; J70332; RDECEP.
DR EcoGene; EG10065; argC.
DR InterPro; IPR000706; AGPR_act_site.
DR InterPro; IPR000534; Semialdh_dh.
DR Pfam; PF01118; Semialdehyde_dh; 1.
DR Pfam; PF02774; Semialdehyde_dhc; 1.
DR ProDom; PD003765; AGPR_act_site; 1.
DR PROSITE; PS01224; ARGC; 1.
DR Arginine biosynthesis; Oxidoreductase; NADP; Complete proteome.
KW ACT_SITE 154 154 BY SIMILARITY.
SQ SEQUENCE 334 AA; 35952 MW; 67AC195ECE1C4789 CRC64;

Query Match 68.9%; Score 31; DB 1; Length 334;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
DB 109 NDATFYFK 116

RESULT 13
OMP_UVBCH STANDARD; PRT; 341 AA.
AC P97085; Q9L5A3; Q9KU90;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein U precursor (Porin ompU).
DE OMPU OR VC0633.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLASSICAL OGAWA 395 / ATCC 39541 / SEROTYPE O1;
RX MEDLINE=97101069; PubMed=8945596;
RA Sperandio V., Bailey C.C., Giron J.A., Dirita V.J., Silveira W.D.,
RA Vettore A.L., Kaper J.B.;
RT "Cloning and characterization of the gene encoding the OmpU outer
RT membrane protein of Vibrio cholerae.";
RL Infect. Immun. 64:5406-5409(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR;
RA Yin Y., Zhang J.Z.;
RT "Cloning and expression of ompU of Vibrio cholerae and its
RT antigenicity analysis.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;

```


Db 290 HDGTFYFK 297

RESULT 15

PAFA_HUMAN

ID PAFA_HUMAN STANDARD; PRT; 441 AA.

AC Q13093; Q15692;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)

DE (PAF acetylhydrolase) (PAF 2-acetylhydrolase) (LPL-associated

DE phospholipase A2) (LPL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine

DE esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase).

GN PLA2G7 OR PAFAH.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.

RC TISSUE=Myeloid;

RX MEDLINE=95214779; PubMed=7700381;

RA Tjoelker L.W., Wilder C., Eberhardt C., Stafford D.M., Dietsch G.,

RA Schimpf B., Hooper S., le Trong H., Cousins L.S., Zimmerman G.A.,

RA Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;

RT "Anti-inflammatory properties of a platelet-activating factor

RT acetylhydrolase.";

RL Nature 374:549-553(1995).

RN [2]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Lymphoma;

RX MEDLINE=96197208; PubMed=8624782;

RA Tew D.G., Southern C., Rice S.Q.J., Lawrence M.P., Li H., Boyd H.F.,

RA Moores K., Gloger I.S., Macphee C.H.;

RT "Purification, properties, sequencing, and cloning of a lipoprotein-

RT associated, serine-dependent phospholipase involved in the oxidative

RT modification of low-density lipoproteins.";

RL Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).

RN [3]

RP MUTAGENESIS.

RX MEDLINE=96029630; PubMed=7592717;

RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,

RA Zimmerman G.A., McIntyre T.M., Stafford D.M., Prescott S.M.,

RA Gray P.W.;

RT "Plasma platelet-activating factor acetylhydrolase is a secreted

RT phospholipase A2 with a catalytic triad.";

RL J. Biol. Chem. 270:25481-25487(1995).

RN [4]

RP VARIANT PHE-279.

RX MEDLINE=96259525; PubMed=8675689;

RA Stafford D.M., Satoh K., Atkinson D.L., Tjoelker L.W.,

RA Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,

RA McIntyre T.M., Gray P.W., Prescott S.M.;

RT "Platelet-activating factor acetylhydrolase deficiency. A missense

RT mutation near the active site of an anti-inflammatory

RT phospholipase.";

RL J. Clin. Invest. 97:2784-2791(1996).

RN [5]

RP VARIANT PLA2G7 DEFICIENCY ARG-281.

RX MEDLINE=97396177; PubMed=9245731;

RA Yamada Y., Yokota M.;

RT "Loss of activity of plasma platelet-activating factor acetylhydrolase

RT due to a novel Gln281-->Arg mutation.";

RL Biochem. Biophys. Res. Commun. 236:772-775(1997).

RN [6]

RP VARIANT PHE-279.

RX MEDLINE=98074100; PubMed=9412624;

RA Hiramoto M., Yoshida H., Imaizumi T., Yoshimizu N., Satoh K.;

RT "A mutation in plasma platelet-activating factor acetylhydrolase

RT (Val279-->Phe) is a genetic risk factor for stroke.";

RL Stroke 28:2417-2420(1997).

RN [7]

RP VARIANT PHE-279.

RX MEDLINE=98132308; PubMed=9472966;

RA Yamada Y., Ichihara S., Fujimura T., Yokota M.;

RT "Identification of the G994-->T missense in exon 9 of the plasma

RT platelet-activating factor acetylhydrolase gene as an independent

RT risk factor for coronary artery disease in Japanese men.";

RL Metabolism 47:177-181(1998).

RN [8]

RP VARIANT PHE-279.

RX MEDLINE=98430412; PubMed=9759612;

RA Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,

RA Yoshimizu N., Fukushi K., Satoh K.;

RT "A mutation in plasma platelet-activating factor acetylhydrolase

RT (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not

RT for hypertension.";

RL Thromb. Haemost. 80:372-375(1998).

RN [9]

RP VARIANTS HIS-92; THR-198 AND ALA-379.

RX MEDLINE=20311534; PubMed=10733466;

RA Kruse S., Mao X.-Q., Heinzmann A., Blattmann S., Roberts M.H.,

RA Braun S., Gao P.-S., Forster J., Kuehr J., Hopkin J.M., Shirakawa T.,

RA Deichmann K.A.;

RT "The Ile198Thr and Ala379Val variants of plasmatic PAF-acetylhydrolase

RT impair catalytical activities and are associated with atopy and

RT asthma.";

RL Am. J. Hum. Genet. 66:1522-1530(2000).

CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)

CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY

CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT

CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN

CC PHOSPHOLIPIDS.

CC -!- CATALYTIC ACTIVITY: 2-acetyl-1-alkyl-sn-glycero-3-phosphocholine +

CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.

CC -!- SUBCELLULAR LOCATION: Extracellular.

CC -!- TISSUE SPECIFICITY: PLASMA.

CC -!- POLYMORPHISM: THE POLYMORPHIC ALLELES THR-198 AND VAL-379 ARE

CC ASSOCIATED WITH ATOPY AND ASTHMA.

CC -!- DISEASE: DEFECTS IN PLA2G7 ARE THE CAUSE OF PLA2G7 DEFICIENCY A

CC TRAIT WHICH IS PRESENT IN 2% OF JAPANESE. IT COULD HAVE A

CC SIGNIFICANT PHYSIOLOGIC EFFECT IN THE PRESENCE OF INFLAMMATORY

CC BODILY RESPONSES.

CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,

CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).

CC -----

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CC -----

CC EMBL; U20157; AAC50126.1; -

CC EMBL; U24577; AAB04170.1; -

CC MIM; 601690; -

CC InterPro: IPR000379; Est_lip_thioest_actsite.

CC InterPro: IPR000734; Lipase.

CC PROSITE; PS00120; LIPASE_SER; 1.

CC Hydrolase; Lipid degradation; Glycoprotein; Signal; Polymorphism;

CC Disease mutation.

CC SIGNAL 1 21

CC CHAIN 22 441 PLATELET-ACTIVATING FACTOR

CC ACT_SITE 273 273 ACETYLHYDROLASE.

CC ACT_SITE 296 296 CHARGE RELAY SYSTEM.

CC ACT_SITE 351 351 CHARGE RELAY SYSTEM.

CC CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 433 433 N-LINKED (GLCNAC. . .)

CC VARIANT 92 92 R -> H (COMMON POLYMORPHISM; IN

CC DBSNP:1805017).

CC VARIANT 198 198 I -> T (COMMON POLYMORPHISM; IN

CC DBSNP:1805018).

```
FT FTid-VAR_011584.
FT V -> F (IN PLA2G7 DEFICIENCY; LOSS OF
FT FUNCTION: MORE COMMON AMONG JAPANESE THAN
FT IN CAUCASIANS; RISK FACTOR FOR CORONARY
FT ARTERY DISEASE AND STROKE).
FT /FTid-VAR_004268.
FT Q -> R (IN PLA2G7 DEFICIENCY; LOSS OF
FT FUNCTION).
FT /FTid-VAR_011585.
FT V -> A (COMMON POLYMORPHISM).
FT /FTid-VAR_011586.
FT S->A: ACTIVITY IS HIGHER THAN WILD TYPE.
FT S->A: LOSS OF ACTIVITY.
FT D->A: ALMOST NO ACTIVITY.
FT D->N: DIMINISHED ACTIVITY.
FT D->A: LOSS OF ACTIVITY.
FT D->N: LOSS OF ACTIVITY.
FT D->A: NO CHANGE IN ACTIVITY.
FT D->A: ACTIVITY IS HIGHER THAN WILD TYPE.
FT H->A: LOSS OF ACTIVITY.
FT SQ SEQUENCE 441 AA; 50077 MW; 3BA9EEA9E8094A57 CRC64;
```

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 77;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFEYFK 8
Db :|||:|
185 SATYIFK 191

Search completed: July 10, 2002, 09:22:11
Job time: 97 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 10, 2002, 09:20:34 ; Search time 25.02 Seconds
(without alignments)
55.314 Million cell updates/sec

Title: US-09-461-061a-1

Perfect score: 45

Sequence: 1 NNATFYFK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_unclassified:*

14: sp_virus:*

15: sp_bacteriophage:*

16: sp_bacteriophage:*

17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 36 | 80.0 | 858 | 5 Q21853 | Q21853 caenorhabdi |
| 2 | 35 | 77.8 | 182 | 5 Q21968 | Q21968 caenorhabdi |
| 3 | 34 | 75.6 | 71 | 16 Q9KDI7 | Q9KDI7 bacillus ha |
| 4 | 34 | 75.6 | 115 | 15 Q9YXT3 | Q9YXT3 human immu |
| 5 | 34 | 75.6 | 173 | 10 Q3RFR8 | Q3RFR8 oryza sativ |
| 6 | 34 | 75.6 | 181 | 10 Q9M625 | Q9M625 hordeum vul |
| 7 | 34 | 75.6 | 182 | 10 Q93615 | Q93615 tritium ae |
| 8 | 34 | 75.6 | 273 | 16 Q9CD90 | Q9CD90 mycobacteri |
| 9 | 34 | 75.6 | 319 | 16 Q9CJ05 | Q9CJ05 lactococcus |
| 10 | 34 | 75.6 | 326 | 12 Q66771 | Q66771 equine rota |
| 11 | 34 | 75.6 | 326 | 12 Q66772 | Q66772 equine rota |
| 12 | 34 | 75.6 | 326 | 12 Q9IE87 | Q9IE87 human rotav |
| 13 | 34 | 75.6 | 357 | 13 Q91655 | Q91655 xenopus lae |
| 14 | 34 | 75.6 | 440 | 8 Q92Y23 | Q92Y23 pedinomonas |
| 15 | 34 | 75.6 | 497 | 10 Q9FVS9 | Q9FVS9 arabidopsis |
| 16 | 34 | 75.6 | 602 | 2 Q9AFA2 | Q9AFA2 staphylococ |

| | | | | | |
|----|----|------|------|-----------|--------------------|
| 17 | 34 | 75.6 | 630 | 5 P91391 | P91391 caenorhabdi |
| 18 | 34 | 75.6 | 758 | 5 O16610 | O16610 caenorhabdi |
| 19 | 34 | 75.6 | 949 | 16 Q97DM1 | Q97DM1 clostridium |
| 20 | 33 | 73.3 | 251 | 10 Q9LDL9 | Q9LDL9 arabidopsis |
| 21 | 33 | 73.3 | 303 | 5 O44623 | O44623 caenorhabdi |
| 22 | 33 | 73.3 | 332 | 10 O64597 | O64597 arabidopsis |
| 23 | 33 | 73.3 | 469 | 17 Q29037 | Q29037 archaeglob |
| 24 | 33 | 73.3 | 706 | 10 Q9S7L6 | Q9S7L6 arabidopsis |
| 25 | 33 | 73.3 | 1346 | 5 O45699 | O45699 caenorhabdi |
| 26 | 32 | 71.1 | 155 | 8 Q79080 | Q79080 lipolexis g |
| 27 | 32 | 71.1 | 331 | 12 Q91AP3 | Q91AP3 human rotav |
| 28 | 32 | 71.1 | 537 | 10 Q9LH23 | Q9LH23 oryza sativ |
| 29 | 32 | 71.1 | 606 | 8 Q9GLW4 | Q9GLW4 sus scrofa |
| 30 | 32 | 71.1 | 606 | 8 Q9TDR1 | Q9TDR1 sus scrofa |
| 31 | 32 | 71.1 | 606 | 8 Q99997 | Q99997 sus scrofa |
| 32 | 32 | 71.1 | 606 | 8 Q9G7T6 | Q9G7T6 sus scrofa |
| 33 | 32 | 71.1 | 606 | 8 Q9G7R8 | Q9G7R8 sus scrofa |
| 34 | 32 | 71.1 | 630 | 12 Q9EML1 | Q9EML1 amsacta moo |
| 35 | 32 | 71.1 | 1096 | 4 Q94836 | Q94836 homo sapien |
| 36 | 32 | 71.1 | 1191 | 5 Q9VJN7 | Q9VJN7 drosophila |
| 37 | 32 | 71.1 | 1215 | 5 Q22649 | Q22649 caenorhabdi |
| 38 | 32 | 71.1 | 1255 | 5 Q9NK83 | Q9NK83 drosophila |
| 39 | 32 | 71.1 | 1560 | 5 Q9GRX5 | Q9GRX5 dictyosteli |
| 40 | 32 | 71.1 | 1561 | 5 Q9U987 | Q9U987 dictyosteli |
| 41 | 32 | 71.1 | 1731 | 5 Q95W43 | Q95W43 trypanosoma |
| 42 | 31 | 68.9 | 49 | 13 Q98TR0 | Q98TR0 gallus gall |
| 43 | 31 | 68.9 | 110 | 11 Q9JLF2 | Q9JLF2 rattus norv |
| 44 | 31 | 68.9 | 118 | 4 Q9UI66 | Q9UI66 homo sapien |
| 45 | 31 | 68.9 | 121 | 15 Q9Q7U5 | Q9Q7U5 human immu |

ALIGNMENTS

RESULT 1

Q21853 PRELIMINARY; PRT; 858 AA.
ID Q21853;
AC Q21853;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE R09A8.2 PROTEIN.
GN R09A8.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z68009; CAA92004.1; -;
SQ SEQUENCE 858 AA; 96262 MW; 60E1070CA8F4D4C8 CRC64;

Query Match 80.0%; Score 36; DB 5; Length 858;
Best Local Similarity 75.0%; Pred. No. 89;
Matches. 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYFK 8

Db 49 NESTFYFK 56

RESULT 2

Q21968

ID Q21968 PRELIMINARY; PRT; 182 AA.
 AC Q21968;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE R12H7.3 PROTEIN.
 GN R12H7.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Coles L.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z50755; CAA90635.1; -;
 DR InterPro; IPR001232; Skp1.
 DR Pfam; PF01466; Skp1; 1.
 DR SMART; SMO0512; Skp1; 1.
 SQ SEQUENCE 182 AA; 21178 MW; 4BE38A19C4FA8124 CRC64;

Query Match 77.8%; Score 35; DB 5; Length 182;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYK 8
 |||||:
 Db 161 NNATLFFK 168

RESULT 3
 ID Q9KDI7 PRELIMINARY; PRT; 71 AA.
 AC Q9KDI7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE BH1226 PROTEIN.
 GN BH1226.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirata C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001511; BAB04945.1; -;
 KW Complete proteome.
 SQ SEQUENCE 71 AA; 8026 MW; 311AC9AEB3C539D3 CRC64;

Query Match 75.6%; Score 34; DB 16; Length 71;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFFYF 7
 |||||
 Db 43 NATFFYF 48

RESULT 4
 ID Q9YXT3 PRELIMINARY; PRT; 115 AA.
 AC Q9YXT3;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN C2V3 REGION (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RJ96BRP071;
 RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
 RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
 RA Rayfield M.;
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF034019; AAC79271.1; -;
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 115
 SQ SEQUENCE 115 AA; 12755 MW; 6551E67B32DCF56C CRC64;

Query Match 75.6%; Score 34; DB 15; Length 115;
 Best Local Similarity 62.5%; Pred. No. 31;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYK 8
 |||||:
 Db 78 NNTTFFFR 85

RESULT 5
 ID Q9ZRF8 PRELIMINARY; PRT; 173 AA.
 AC Q9ZRF8;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYDROPHOBIC LEA-LIKE PROTEIN.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L0MELLO;
 RA Chen L.J., Chai Y.J., Chen P.W.;
 RT "A rice embryo-specific gene with high homology to soybean GmPM3 gene,
 RT a hydrophobic LEA protein gene.";
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U57639; AAD10377.1; -;
 SQ SEQUENCE 173 AA; 18287 MW; 63FA2F778BB7259D CRC64;

Query Match 75.6%; Score 34; DB 10; Length 173;
 Best Local Similarity 85.9%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYF 7
 |||||
 Db 47 NGATFFYF 53

```

RESULT 6
ID Q9M625 PRELIMINARY; PRT; 181 AA.
AC Q9M625;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE PLASMA MEMBRANE ASSOCIATED PROTEIN.
GN PM19.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Morris P.C., Ranford J.C.; "Hordeum vulgare hydrophobic embryo-associated protein PM19 mRNA.";
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF218627; AAF29532.1; -.
DR EMBL; AF218627; AAF29532.1; -.
SQ SEQUENCE 181 AA; 19036 MW; 849727F1123A4030 CRC64;

Query Match 75.6%; Score 34; DB 10; Length 181;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATYFF 7
DB 47 NGATYFF 53

RESULT 7
ID P93615 PRELIMINARY; PRT; 182 AA.
AC P93615;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE ABA INDUCED PLASMA MEMBRANE PROTEIN PM 19.
GN WTABAPW.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. CHIHOKU;
RX MEDLINE=97393494; PubMed=9249988;
RA Koike M., Takezawa D., Arakawa K., Yoshida S.;
RT "Accumulation of 19-kDa plasma membrane polypeptide during induction
of freezing tolerance in wheat suspension-cultured cells by abscisic
acid.";
RL Plant Cell Physiol. 38:707-716(1997).
DR EMBL; U80037; AAB38504.1; -.
SQ SEQUENCE 182 AA; 19009 MW; 799B99994AEA87DCB CRC64;

Query Match 75.6%; Score 34; DB 10; Length 182;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATYFF 7
DB 47 NGATYFF 53

RESULT 8
ID Q9CD90 PRELIMINARY; PRT; 273 AA.
AC Q9CD90;
DT 01-JUN-2001 (TRENBLrel. 17, Created)

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DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
DE HYPOTHETICAL PROTEIN ML0126.
GN ML0126.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Felwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
DR EMBL; AL583917; CAC29634.1; -.
DR Leproma; ML0126; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 273 AA; 30831 MW; D5B765A65EF39549 CRC64;

Query Match 75.6%; Score 34; DB 16; Length 273;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATYFF 7
DB 20 NNAQYFF 26

RESULT 9
Q9CJ05 PRELIMINARY; PRT; 319 AA.
AC Q9CJ05;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE RHAMNOSYLTRANSFERASE.
GN RGPB.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
DR EMBL; AE006258; AAK04299.1; -.
DR HSP; P39621; ICG8.
DR InterPro; IPR001173; Glycos_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 319 AA; 37340 MW; DIDAC78AB0A950CA CRC64;

Query Match 75.6%; Score 34; DB 16; Length 319;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATYFF 7

```

Db 80 NNADEYF 86
||| |||

RESULT 10

Q66771 ID Q66771 PRELIMINARY; PRT; 326 AA.
AC Q66771;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GLYCOPROTEIN VP7.
OS Equine rotavirus.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10937;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FR4;
RX MEDLINE=95113988; PubMed=7814511;
RA Charlet M., Reggati F., Pina C.I., Liprandi F.,
RT "Equine rotaviruses with G14 serotype specificity circulate among
RT Venezuelan horses"; 32:2609-2612(1994).
RL J. Clin. Microbiol. 32:2609-2612(1994).
DR EMBL; U05348; AAA81914.1; -;
DR InterPro; IPR001963; VP7.
DR Pfam; PF00434; VP7; 1.
SQ SEQUENCE 326 AA; 37296 MW; 9FC1BD4F4CC76529 CRC64;

Query Match 75.6%; Score 34; DB 12; Length 326;
Best Local Similarity 62.5%; Pred. No. 84;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNADEYF 8
|:|||||:
Db 318 NSATFYFR 325

RESULT 11

Q66772 ID Q66772 PRELIMINARY; PRT; 326 AA.
AC Q66772;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GLYCOPROTEIN VP7.
OS Equine rotavirus.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10937;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FR8;
RX MEDLINE=95113988; PubMed=7814511;
RA Charlet M., Reggati F., Pina C.I., Liprandi F.,
RT "Equine rotaviruses with G14 serotype specificity circulate among
RT Venezuelan horses"; 32:2609-2612(1994).
RL J. Clin. Microbiol. 32:2609-2612(1994).
DR EMBL; U05349; AAA67342.1; -;
DR InterPro; IPR001963; VP7.
DR Pfam; PF00434; VP7; 1.
SQ SEQUENCE 326 AA; 37352 MW; 9095E64B13933E29 CRC64;

Query Match 75.6%; Score 34; DB 12; Length 326;
Best Local Similarity 62.5%; Pred. No. 84;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNADEYF 8
|:|||||:
Db 318 NSATFYFR 325

RESULT 12

Q91E87

ID Q91E87 PRELIMINARY; PRT; 326 AA.
AC Q91E87;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CAPSID PROTEIN.
GN VP7.
OS Human rotavirus.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CC425, P3[9],G3;
RA Griffin D.D., Nakagomi T., Hoshino Y., Nakagomi O., Kirkwood C.D.,
RA Parashar U.D., Glass R.I., Gentsch J.R.;
RT "Characterization of nontypeable rotavirus strains from the United
RT States: identification of a new rotavirus reassortant (P2A[6],G12) and
RT rare P3[9] strains related to bovine rotaviruses.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ311738; CAC43312.1; -;
SQ SEQUENCE 326 AA; 37119 MW; 8B97ED1DBBD1C981 CRC64;

Query Match 75.6%; Score 34; DB 12; Length 326;
Best Local Similarity 62.5%; Pred. No. 84;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNADEYF 8
|:|||||:
Db 318 NSATFYFR 325

RESULT 13

Q91655 ID Q91655 PRELIMINARY; PRT; 357 AA.
AC Q91655;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GENE 17 PROTEIN.
GN GENE 17.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96312514; PubMed=8700860;
RA Brown D.D., Wang Z., Furrow J.D., Kanamori A., Schwartzman R.A.,
RA Remo B.F., Pinder A.;
RT "The thyroid hormone-induced tail resorption program during Xenopus
RT laevis metamorphosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1924-1929(1996).
DR EMBL; U41860; AAC59876.1; -;
DR InterPro; IPR001507; zona_pellucida.
DR Pfam; PF00100; zona_pellucida; 1.
DR SMART; SM00241; ZP; 1.
SQ SEQUENCE 357 AA; 39090 MW; 5493352C8EFA21E6 CRC64;

Query Match 75.6%; Score 34; DB 13; Length 357;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNADEYF 7
|:|||||:
Db 141 NNATLYF 147

RESULT 14

Q92Y23

ID Q92Y23 PRELIMINARY; PRT; 440 AA.
AC Q92Y23;
DT 01-WAY-1999 (TREMBlrel. 10, Created)
DT 01-WAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT 2 (EC 1.6.5.3).
GN NAD2.
OS Pedinomonas minor.
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Chlorophyta; Pedinophyceae; Pedinomonadales;
OC Pedinomonadaceae; Pedinomonas.
OX NCBI_TaxID=3159;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-UTEX LB 1350;
RX MEDLINE=99418884; PubMed=10488238;
RA Turnell M., Lemieux C., Burger G., Lang B.F., Otis C., Plante I.,
RA Gray M.W.;
RT "The complete mitochondrial DNA sequences of Nephroselmis olivacea and
RT Pedinomonas minor: two radically different evolutionary patterns
RT within green algae.";
RL Plant Cell 11:1717-1729(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-UTEX LB 1350;
RA Burger G.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DDJ databases.
CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
DR EMBL; AF116775; AAD19671.1; -;
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 440 AA; 51380 MW; C6D6CBAD72549B4C CRC64;

Query Match 75.6%; Score 34; DB 8; Length 440;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNATFF 7
Db 238 NNATFF 244

RESULT 15
Q9FVS9 PRELIMINARY; PRT; 497 AA.
ID Q9FVS9;
AC Q9FVS9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME P450, PUTATIVE.
GN T8L23.21.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu X.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana";
RL Nature 408:816-820(2000).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AC079733; AAG50737.1; -;
DR InterPro; IPR001128; CYP450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN1.
KW Heme: Hypothetical protein; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 497 AA; 57696 MW; COA37BA59164AB78 CRC64;

Query Match 75.6%; Score 34; DB 10; Length 497;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 NATFFK 8
Db 64 NLTFYFK 70

Search completed: July 10, 2002, 09:22:44
Job time: 130 sec

